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OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 12:33:05 ; Search time 1725.82 Seconds

(Without alignments)
1214.912 Million cell updates/sec

Title: US-09-380-682-2

Perfect score: 591
1 ATGCAGTGCAGACCTCCGGA.....AGTCATCATCCGACAA 591

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 12197726 seqs, 1773875003 residues

Total number of hits satisfying chosen parameters: 24395452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents.NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591	100.0	591	17	US-09-380-682-2
2	583	98.6	591	17	US-09-380-682-18
3	581.4	98.4	591	17	US-09-380-682-16
4	579.8	98.1	591	17	US-09-380-682-12
5	578.2	97.8	591	17	US-09-380-682-10
6	573.4	97.0	591	17	US-09-380-682-14
7	447.2	75.7	6801	5	US-08-126-505A-12
8	447.2	75.7	6951	14	US-09-023-655-1265
9	436.2	73.8	7028	18	US-09-471-275-1933
10	436.2	73.8	7028	18	US-09-496-914A-6567
11	431.2	73.0	574	48	US-60-234-446-1627
12	424.8	71.9	574	48	US-60-234-446-1612
13	406.8	68.8	6938	17	US-09-359-922-358
14	406.8	68.8	6938	17	US-09-359-922-357
15	270.4	45.8	837	24	US-09-716-475-3923
16	267.4	45.2	667	48	US-09-471-275-1975
17	252.6	42.7	398	18	US-60-234-446-1613
18	247.4	41.9	420	16	US-09-289-768-34927
19	239.8	40.6	391	19	US-09-515-128-19608
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22	239.8	40.6	476	17	US-09-359-922-357
23	239.8	40.6	476	17	US-09-359-922-357
24	225	38.1	228	17	US-09-380-682-30
25	217	36.7	228	17	US-09-380-682-28
26	215.4	36.4	228	17	US-09-380-682-26
27	213.8	35.2	228	17	US-09-380-682-22
28	212.2	35.9	228	17	US-09-380-682-20
29	207.4	35.1	228	17	US-09-380-682-24
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33	168	28.4	630	42	US-60-177-507-1243
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35	166.8	28.2	467	39	US-60-147-499-18977
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37	166.2	28.1	470	17	US-09-353-690-4138
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40	164.6	27.9	217	48	US-60-234-446-1625
41	164.6	27.9	9276	48	US-60-234-446-1617
42	163	27.6	2644	48	US-60-234-446-432
43	161	27.2	723	43	US-60-188-162-1554
44	161	27.2	723	43	US-60-188-162-1555
45	161	27.2	723	43	US-60-188-162-2514

ALIGNMENTS

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RESULT 1
US-09-380-682-2
; Sequence 2, Application US/09380682
; GENERAL INFORMATION:
; APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena
; COX, Vivienne Frances
; SMITH, Richard Anthony Godwin
; TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE
; SEQUENCES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,682
; FILING DATE: 19-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB98/00727
; FILING DATE: 05-MAR-1998
; APPLICATION NUMBER: GB 9704519.9
; FILING DATE: 05-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 88362/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-380-682-2
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Best Local Similarity 100.0%; Pred. No. 1,2e-180;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATCAGGCAACCTCCGGAATGCTGCGCGCCGACCAACTGACTGATGAA 60

QY 61 TTGAGTCCGATCGGTACTGCTGACTAGGAATGCCGGGTATTACGGCGC 120
   |||||||
DB 61 TTGAGTCCGATCGGTACTGCTGACTAGGAATGCCGGGTATTACGGCGC 120

QY 121 CCGTTTCTATCATCTGCGCTGAAAACTGTGTGACTGCTAAGACCGTTGCCA 180
   |||||||
DB 121 CCGTTTCTATCATCTGCGCTGAAAACTGTGTGACTGCTAAGACCGTTGCCA 180

QY 181 CGTAAATCTGTGATATCCGCAAGATCCGGTTAAGGCATGTGATCAAGGC 240
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DB 181 CGTAAATCTGTGATATCCGCAAGATCCGGTTAAGGCATGTGATCAAGGC 240

QY 241 ATCCAGTGGTCCCAATTAATATCTTGTACTAAGGTTACCGTGTGATGTTCC 300
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QY 301 TCCAGCGCTACATCATCTCTGTGATGATGTCATTTGGATAATGAACCCGATT 360
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DB 301 TCCAGCGCTACATCATCTCTGTGATGATGTCATTTGGATAATGAACCCGATT 360

QY 361 TGTACCGAATTCGTGTGCTGCGCGCGGACCATGCGCAACGGTGTACCTGTATC 420
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DB 361 TGTACCGAATTCGTGTGCTGCGCGCGGACCATGCGCAACGGTGTACCTGTATC 420

QY 421 AGTCGAGATATTTTCACTATGTTCTGTGTGACCTACCACTGCAATCGGTAGCCGT 480
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DB 421 AGTCGAGATATTTTCACTATGTTCTGTGTGACCTACCACTGCAATCGGTAGCCGT 480

QY 481 GGTAAAAAGTGTGAGCTGCTGGGTGAGCGCGTCCATCTACTGCACTAACAAGAGAT 540
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DB 481 GGTAAAAAGTGTGAGCTGCTGGGTGAGCGCGTCCATCTACTGCACTAACAAGAGAT 540

QY 541 CAAGTGGCATCTGGAGCGCGCGGACCGCATGATCATCCCAACAA 591
DB 541 CAAGTGGCATCTGGAGCGCGCGGACCGCATGATCATCCCAACAA 591
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RESULT 2
US-09-380-682-18
; Sequence 18, Application US/09380682
; GENERAL INFORMATION:
; APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena
; COX, Vivienne Frances
; SMITH, Richard Anthony Godwin
; TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE
; SEQUENCES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,682
; FILING DATE: 19-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB98/00727
; FILING DATE: 05-MAR-1998
; APPLICATION NUMBER: GB 9704519.9
; FILING DATE: 05-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 88362/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-380-682-18
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Query Match      98.6%; Score 583; DB 17; Length 591;
Best Local Similarity 99.2%; Pred. No. 4,6e-178;
Matches 586; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Tue Jan 16 09:11:51 2001

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CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,682
FILING DATE: 19-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB98/00727
FILING DATE: 05-MAR-1998
APPLICATION NUMBER: GB 9704519.9
FILING DATE: 05-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: ISAACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 88362/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 591 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-380-682-12

Query Match 98.1%; Score 579.8; DB 17; Length 591;

Best Local Similarity 98.8%; Pred. No. 5e-177; Mismatches 7; Indels 0; Gaps 0;

Matches 584; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGAGTGCACAGCTCCGGAATGCTGCGCGCCGCGACCACTGATGAA 60
DB 1 ATGAGTGCACAGCTCCGGAATGCTGCGCGCCGCGACCACTGATGAA 60
QY 61 TTGAGTCCGATCGGTACTGACTGAGTGAATGCGCGCGGTTATAGCGCGC 120
DB 61 TTGAGTCCGATCGGTACTGACTGAGTGAATGCGCGCGGTTATAGCGCGC 120
QY 121 CCGTTTCTATCATCTGCTGAAAACTGCTGTGAGTGGTCTAAGACCGTTGCCGA 180
DB 121 CCGTTTCTATCATCTGCTGAAAACTGCTGTGAGTGGTCTAAGACCGTTGCCGA 180
QY 181 CGTAATCTTGTGTAATCCGCAAGATCCGTTAAGCGCATGTCATGATCAAGGC 240
DB 181 CGTAATCTTGTGTAATCCGCAAGATCCGTTAAGCGCATGTCATGATCAAGGC 240
QY 241 ATCCAGTCCGTTCCCAATTAATATCTGTGACTAAGGTACCGTGTATGCTCC 300
DB 241 ATCCAGTCCGTTCCCAATTAATATCTGTGACTAAGGTACCGTGTATGCTCC 300
QY 301 TCCAGCGGTACATCATCTGTGTGATGATGTCATTGSGATGAAGAACCGATT 360
DB 301 TCCAGCGGTACATCATCTGTGTGATGATGTCATTGSGATGAAGAACCGATT 360
QY 361 TGTGACCAATTCGTTGGTGTGCGCGGACCATGCGCAAGGATTTACCTATC 420
DB 361 TGTGACCAATTCGTTGGTGTGCGCGGACCATGCGCAAGGATTTACCTATC 420
QY 421 AGTGGCAATTTTCTACATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 480
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QY 481 GGTAAAAAGTGTGAGCTGCTGGTGAACCGTCCATCTAGTGAAGCAAGAGAT 540
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QY 541 CAATGGGATCTGGAGCGCGCGGACCGCATGATATCCGACAAA 591
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RESULT 5

US-09-380-682-10
Sequence 10, Application US/09380682

GENERAL INFORMATION:

APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena
COX, Vivienne Frances
SMITH, Richard Anthony Godwin

TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE
SEQUENCES

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,682
FILING DATE: 19-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB98/00727
FILING DATE: 05-MAR-1998
APPLICATION NUMBER: GB 9704519.9
FILING DATE: 05-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: ISAACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 88362/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 591 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-380-682-10

Query Match 97.8%; Score 578.2; DB 17; Length 591;

Best Local Similarity 98.6%; Pred. No. 1.6e-176; Mismatches 8; Indels 0; Gaps 0;

Matches 583; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ATGAGTGCACAGCTCCGGAATGCTGCGCGCCGCGACCACTGATGAA 60
DB 1 ATGAGTGCACAGCTCCGGAATGCTGCGCGCCGCGACCACTGATGAA 60
QY 61 TTGAGTCCGATCGGTACTGACTGAGTGAATGCGCGCGGTTATAGCGCGC 120
DB 61 TTGAGTCCGATCGGTACTGACTGAGTGAATGCGCGCGGTTATAGCGCGC 120
QY 121 CCGTTTCTATCATCTGCTGAAAACTGCTGTGAGTGGTCTAAGACCGTTGCCGA 180
DB 121 CCGTTTCTATCATCTGCTGAAAACTGCTGTGAGTGGTCTAAGACCGTTGCCGA 180


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Db 121 CCGTTTCATCATCTGCTGAAAAACCTGCTGTGACGTCGTCCTAGGACCGTTCCCA 180
Qy 181 CGTAATCTTGTGTAATCCGCCAGATCCGGTTAACGGCATGGTGCATGTGATCAAGGC 240
Db 181 CCGTAATCTTGTGTAATCCGCCAGATCCGGTTAACGGCATGGTGCATGTGATCAAGGC 240
Qy 241 ATCCAGTTCGGTCCCAATTAATTTCTGTGACTAAAGTTACCGTGTGATGGTTCG 300
Db 241 ATCCAGTTCGGTCCCAATTAATTTCTGTGACTAAAGTTACCGTGTGATGGTTCG 300
Qy 301 TCCAGCGCTACATGATCATCTCTGTGTGATACGTCATTGGATATGAACACCGATT 360
Db 301 TCCAGCGCTACATGATCATCTCTGTGTGATACGTCATTGGATATGAACACCGATT 360
Qy 361 TGTGACCGAATTCGGTGTGCTGCGCGGACCATGCGCAACGGTATTCACCTCTATC 420
Db 361 TGTGACCGAATTCGGTGTGCTGCGCGGACCATGCGCAACGGTATTCACCTCTATC 420
Qy 421 ACTCGGATATTTTACATATGTTGTGTGTGACCTACCATGCAATCGGTAGCCGT 480
Db 421 ACTCGGATATTTTACATATGTTGTGTGTGACCTACCATGCAATCGGTAGCCGT 480
Qy 481 GGTAAAGAGTGTGAGTCCGTGCGGCGGACCATGCGCAACGGTATTCACCTCTATC 540
Db 481 GGTAAAGAGTGTGAGTCCGTGCGGCGGACCATGCGCAACGGTATTCACCTCTATC 540
Qy 541 CAAGTGGGATCTGAGCGCGCGGACCGACGAGTGCATATCCGAACAA 591
Db 541 CAAGTGGGATCTGAGCGCGCGGACCGACGAGTGCATATCCGAACAA 591
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RESULT 6
US-09-380-682-14
Sequence 14, Application US/09380682

GENERAL INFORMATION:

APPLICANT: MOSAKOWSKA, Danuta Ewa Irena

COX, Vivienne Frances

SMITH, Richard Anthony Godwin

TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,682

FILING DATE: 19-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB98/00727

FILING DATE: 05-MAR-1998

APPLICATION NUMBER: GB 9704519.9

FILING DATE: 05-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: ISACSON, John P.

REGISTRATION NUMBER: 33,715

REFERENCE/DOCKET NUMBER: 88362/107

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 591 base pairs

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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-380-682-14
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Query Match 97.0%; Score 573.4; DB 17; Length 591;
Best Local Similarity 98.1%; Pred. No. 5,9e-175;
Matches 580; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy 1 ATGCAAGTGAAGCTCCGGAATGCGTCCGTCGGCGCCGACCAACCTGATGAA 60
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Db 61 TTTGAGTTCCTGATGCTGCTGAAACCTGCTGTGAGACTGTCTAAGAGCCGTTGCCA 120
Qy 121 CCGTTTCTATCATCTGCTGAAACCTGCTGTGAGACTGTCTAAGAGCCGTTGCCA 180
Db 121 CCGTTTCTATCATCTGCTGAAACCTGCTGTGAGACTGTCTAAGAGCCGTTGCCA 180
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Db 181 CGTAATCTTGTGTAATCCGCCAGATCCGGTTAACGGCATGGTGCATGTGATCAAGGC 240
Qy 241 ATCCAGTTCGGTCCCAATTAATTTCTGTGACTAAAGTTACCGTGTGATGGTTCG 300
Db 241 ATCCAGTTCGGTCCCAATTAATTTCTGTGACTAAAGTTACCGTGTGATGGTTCG 300
Qy 301 TCCAGCGCTACATGATCATCTCTGTGTGATACGTCATTGGATATGAACACCGATT 360
Db 301 TCCAGCGCTACATGATCATCTCTGTGTGATACGTCATTGGATATGAACACCGATT 360
Qy 361 TGTGACCGAATTCGGTGTGCTGCGCGGACCATGCGCAACGGTATTCACCTCTATC 420
Db 361 TGTGACCGAATTCGGTGTGCTGCGCGGACCATGCGCAACGGTATTCACCTCTATC 420
Qy 421 ACTCGGATATTTTACATATGTTGTGTGTGACCTACCATGCAATCGGTAGCCGT 480
Db 421 ACTCGGATATTTTACATATGTTGTGTGTGACCTACCATGCAATCGGTAGCCGT 480
Qy 481 GGTAAAGAGTGTGAGTCCGTGCGGCGGACCATGCGCAACGGTATTCACCTCTATC 540
Db 481 GGTAAAGAGTGTGAGTCCGTGCGGCGGACCATGCGCAACGGTATTCACCTCTATC 540
Qy 541 CAAGTGGGATCTGAGCGCGCGGACCGACGAGTGCATATCCGAACAA 591
Db 541 CAAGTGGGATCTGAGCGCGCGGACCGACGAGTGCATATCCGAACAA 591
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RESULT 7
US-08-126-505A-12

Sequence 12, Application US/08126505A

GENERAL INFORMATION:

APPLICANT: Alkinson, John P.

APPLICANT: Hourcade, Dennis

TITLE OF INVENTION: Modified Truncated Complement System

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Babst

STREET: 2800 One Atlantic Center, 1201 West Peachtree

CITY: Atlanta

STATE: Georgia

COUNTRY: US

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

```

/
/  COMPUTER: IBM PC compatible
/  OPERATING SYSTEM: PC-DOS/MS-DOS
/  SOFTWARE: PatentIn Release #1.0, Version #1.25
/  CURRENT APPLICATION DATA:
/  APPLICATION NUMBER: US/08/126,505A
/  FILING DATE: 24-SEP-1993
/  CLASSIFICATION: 435
/  PRIORITY APPLICATION DATA:
/  APPLICATION NUMBER: US 07/695,514
/  FILING DATE: 03-MAY-1991
/  ATTORNEY/AGENT INFORMATION:
/  NAME: Padst, Patrea L.
/  REGISTRATION NUMBER: 31,284
/  REFERENCE/DOCKET NUMBER: WU101CIP
/  TELECOMMUNICATION INFORMATION:
/  TELEPHONE: (404)873-8794
/  TELEFAX: (404)873-8795
/  INFORMATION FOR SEQ ID NO: 12:
/  SEQUENCE CHARACTERISTICS:
/  LENGTH: 6801 base pairs
/  TYPE: nucleic acid
/  STRANDEDNESS: double
/  TOPOLOGY: linear
/  MOLECULE TYPE: cDNA to mRNA
/  FEATURE:
/  NAME/KEY: CDS
/  LOCATION: 1..5994
/  US-08-126-505A-12

```

```

Query Match      75.7%; Score 447.2; DB 5; Length 6801;
Best Local Similarity 85.0%; Pred. No. 1.4e-133;
Matches 500; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 4 CAGTGCACGCTCCGGAATGCTGCGCGCGCGCCGACCACTGACGATGATTT 63
DB 1 CAATGCAATGCCCAAGATGGCTTCATTTGCCAGGCTTACCACTGACGATGATTT 60
QY 64 GAGTCCCGATGGTACCTACTGAACTAGCAATGCCCGCGGTTATAGGCGCGCCG 123
DB 61 GAGTTCCTCATTTGGGACATATCTGAACTATGATCCGCCCTGGTTATTCGGGAAGCG 120
QY 124 TTTTCTATCATCTGCTGAAAAAACTCTGTGAGATGCTGTGCTAAGACCGTGGCGAGT 183
DB 121 TTTTCTATCATCTGCTGAAAAAACTCACTGAGTGTGAGTGTGCTAAGACCGTGGCGAGT 180
QY 184 AAATCTGTGCTGATCCGCCAGATCCGGTTAAGCGCATGTCATGTGATCAAGGATC 243
DB 181 AAATCATGTGCTGATCCGCCAGATCCGTGTGATGCGATGTCATGTGATCAAGGATC 240
QY 244 CAGTTCGCTCCCAAAATTAATTTCTGTACTAAAGTTACGCTGATTTGTTCTCC 303
DB 241 CAGTTCGCTCCCAAAATTAATTTCTGTACTAAAGTTACGCTGATTTGTTCTCC 300
QY 304 AGCGCTATCATCATCTGCTGTGATGATCTGCTATTTGGGATATGAAACCGATTTGT 363
DB 301 TCTCCACATCATCATCTGCTGTGATGATCTGCTATTTGGGATATGAAACCGATTTGT 360
QY 364 GACCGAATTCGCTGTGCTGCGCGCGCCAGCATGCCACGAGTATTTACCTTATCACT 423
DB 361 GACAGAAATTCCTTGTGGCTACCCGCCACCATCACAATGAGATTTCAATTACACCAAC 420
QY 424 CGCAGATTTTCACTATGTTCTGTGATGATCTGCTACCATGCAATGCGGTAGCGCTGT 483
DB 421 AGAGAGATTTTCACTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 484 AAAAGGTTTGTAGCGCTGCGGTGAGCGCTCATCTATCTGCTAGCAAGACGATCAA 543
DB 481 AGAAAGGTTTGTAGCGCTGCGGTGAGCGCTCATCTATCTGCTAGCAAGACGATCAA 540
QY 544 GTGGGATCTGAGCGCGCGCGCGCGAGTGCATCATCCGACCAAA 591
DB 541 GTGGGATCTGAGCGCGCGCGCGCGCTCAGTGCATTAATCACTAAGAAA 588

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RESULT
8
US-09-023-655-1265
/ Sequence 1265, Application US/09023655
/ GENERAL INFORMATION:
/ APPLICANT: Cocks, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ APPLICANT: Jeffrey J. Sellhammer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1265:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6951 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: 930185
/ US-09-023-655-1265

Query Match      75.7%; Score 447.2; DB 14; Length 6951;
Best Local Similarity 85.0%; Pred. No. 1.4e-133;
Matches 500; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 4 CAGTGCACGCTCCGGAATGCTGCGCGCGCGCCGACCACTGACGATGATTT 63
DB 151 CAATGCAATGCCCAAGATGGCTTCATTTGCCAGGCTTACCACTGACGATGATTT 210
QY 64 GAGTTCCTCATTTGGGACATATCTGAACTATGATGCTGCTGATTTTCCGGAAGACCG 123
DB 211 GAGTTCCTCATTTGGGACATATCTGAACTATGATGCTGCTGATTTTCCGGAAGACCG 270
QY 124 TTTTCTATCATCTGCTGAAAAAACTGTCTGAGATGCTGTGCTAAGGACCGTGGCGAGT 183
DB 271 TTTTCTATCATCTGCTGAAAAAACTGTCTGAGATGCTGTGCTAAGGACCGTGGCGAGT 180
QY 184 AAATCTGTGCTGATCCGCCAGATCCGGTTAAGCGATGTCATGTGATCAAGGATC 243
DB 331 AAATCATGTGCTGATCCGCCAGATCCGTGTGATGCGATGTCATGTGATCAAGGATC 390
QY 244 CAGTTCGCTCCCAAAATTAATTTCTGTACTAAAGTTACGCTGATTTGTTCTCC 303

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Db 391 CAGTCGGATCCCAATTAATATCTTGTACTAAGGATACCGACTCATTGGTCTCG 450
QY 304 AGCGCTACATGCATCTCTGTGTGATCTGATTTGGGATATGAACACCGATTGT 363
Db 451 TCTGCACATGCATCTCTGTGTGATCTGATTTGGGATATGAACACCGATTGT 510
QY 364 GACCGAATTCGGTGTGTGCGCGACCGACCATGGCCAAAGGTGATTTCACTATCAGT 423
Db 511 GACGAAATTCCTTGTGGGCTACCCGCCACCATCAACATGAGATTTTATAGCACCAAC 570
QY 424 CCGGATATTTTCACTATGTTCTGTGTGATCTGATCTGATTTGGGATATGAACACCGATTGT 483
Db 571 AGAGAAATTTTCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 630
QY 484 AAAAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
Db 631 AGAAAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 690
QY 544 GTGGGATCTGGAGCGCGCGCGACCGACCATGATCATCCGAAACAA 591
Db 691 GTGGGATCTGGAGCGCGCGCGCGACCGACCATGATCATCCGAAACAA 738

```

RESULT 9

```

US-09-471-275-1933
; Sequence 1933, Application US/09471275
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 782
; CURRENT APPLICATION NUMBER: US/09/471,275
; EARLIER FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: US 09/235,076
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: US 09/234,611
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: US 09/240,371
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: US 09/277,227
; EARLIER FILING DATE: 1999-03-25
; EARLIER APPLICATION NUMBER: US 09/271,490
; EARLIER FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: US 09/293,972
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 09/274,861
; EARLIER FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: US 60/125,453
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/126,605
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: US 09/306,350
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/399,720
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: US 09/404,284
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 10451
; SOFTWARE: pt_CT_genes Version 1.0
; SEQ ID NO 1933
; LENGTH: 7028
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)...(6148)
; OTHER INFORMATION: similar to g130186 in the genepept database release 114,
US-09-471-275-1933

```

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Query Match 73.8%; Score 436.2; DB 18; Length 7028;
Best Local Similarity 84.9%; Pred. No. 5,2e-130;
Matches 500; Conservative 0; Mismatches 88; Indels 1; Gaps 1;

QY 4 CAGTGAACGCTCCGGAAT-GGCTGCCGTCGCGCCCGACCACTGATGATGAT 62
Db 151 caatgcaatgccccaaatgggtcttcatttgcacagcctaccacttaactatgagt 210
QY 63 TGAGTTCGCGATGGATACCTACCTGAACGATGATGATGATGATGATGATGATGATGAT 122
Db 211 tgaattccattgggacatatctgactatgactatgactatgactatgactatgactatgact 270
QY 123 GTTTTCTATATCTGCTGAAAACCTCTGTGTGATGATGATGATGATGATGATGATGATGAT 182
Db 271 gtcttcatatctgcttcaaaaactcagctgactgactgactgactgactgactgactgact 330
QY 183 TAAATCTTGCTATATCCGACGATCCGCTTAACGCGATGATGATGATGATGATGATGATGAT 242
Db 331 taatcatgctgtaactcccaagatccctgtgactgactgactgactgactgactgactgact 390
QY 243 CCAATTCGCTTCCCAATTAATATCTTGTACTAAGGATTAACGCTGATGATGATGATGATGAT 302
Db 391 ccagttcggatcccaaatataatattctgtacttaagaagatccgactcattgttccctc 450
QY 303 CACGCTACATGCATCTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 362
Db 451 gtctgcacatgactatcctcagctgactgactgactgactgactgactgactgactgact 510
QY 363 TGACGGAATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
Db 511 tgaagaatccctgtggtggtaccccccacacacacacacacacacacacacacacacac 570
QY 423 TCGGAGATTTTCACTATGTTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 482
Db 571 cagagaagaatttcactatgactcagtggtgactcagtggtgactcagtggtgactcagtggt 630
QY 483 TAAAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 542
Db 631 gagaagaagtgttgaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 690
QY 543 AGTGGCATCTGGAGCGCGCGCGACCGACGATCATCCGAAACAA 591
Db 691 agtggcatctggagcgcgcccgccctcagtgactatataccaacaa 738

RESULT 10
US-09-496-914A-6567
; Sequence 6567, Application US/09496914A
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Slinko, Arkura
; APPLICANT: Liu, Chenhua
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 787
; CURRENT APPLICATION NUMBER: US/09/496,914A
; EARLIER FILING DATE: 2000-02-03
; EARLIER APPLICATION NUMBER: US 09/353,690
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: US 09/034,341
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: US 09/045,400
; EARLIER FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: US 09/321,214
; EARLIER FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: US 09/131,598
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: US 09/431,517
; EARLIER FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: US 09/328,351
; EARLIER FILING DATE: 1999-06-04

```

```

: PRIOR APPLICATION NUMBER: US 09/332,782
: PRIOR FILING DATE: 1999-06-14
: PRIOR APPLICATION NUMBER: US 09/235,076
: PRIOR FILING DATE: 1999-01-20
: PRIOR APPLICATION NUMBER: US 09/234,611
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: US 09/346,956
: PRIOR FILING DATE: 1999-07-02
: PRIOR APPLICATION NUMBER: US 09/362,510
: PRIOR FILING DATE: 1999-07-27
: PRIOR APPLICATION NUMBER: US 09/240,371
: PRIOR FILING DATE: 1999-01-29
: PRIOR APPLICATION NUMBER: US 09/248,797
: PRIOR FILING DATE: 1999-02-12
: PRIOR APPLICATION NUMBER: US 09/271,490
: PRIOR FILING DATE: 1999-03-18
: PRIOR APPLICATION NUMBER: US 09/293,972
: PRIOR FILING DATE: 1999-04-15
: PRIOR APPLICATION NUMBER: US 09/274,861
: PRIOR FILING DATE: 1999-03-23
: PRIOR APPLICATION NUMBER: US 60/125,453
: PRIOR FILING DATE: 1999-03-19
: PRIOR APPLICATION NUMBER: US 60/126,605
: PRIOR FILING DATE: 1999-03-26
: PRIOR APPLICATION NUMBER: US 09/306,350
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: US 09/399,720
: PRIOR FILING DATE: 1999-09-21
: PRIOR APPLICATION NUMBER: US 09/404,284
: PRIOR FILING DATE: 1999-09-21
: PRIOR APPLICATION NUMBER: US 09/465,877
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: NOT YET ASSIGNED
: PRIOR FILING DATE: 1999-01-19
: NUMBER OF SEQ ID NOS: 10410
: SOFTWARE: PL CT, genes Version 1.02
: SEQ ID NO 6567
: LENGTH: 7028
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (28)...(6148)
: OTHER INFORMATION: similar to g130186 in the genepept database release 114,
: OTHER INFORMATION: Run with FASTXV 3.3f00, default parameters
US-09-496-914A-6567

```

```

Query Match      73.8%; Score 436.2; DB 18; Length 7028;
Best Local Similarity 84.9%; Pred. No. 5.2e-130;
Matches 500; Conservative 0; Mismatches 88; Indels 1; Gaps 1;

```

```

QY 4 CAGTGAACGCTCCGGGAT-6GCTGCGGTTCGCGCCCGGACCAACCTGATGATAT 62
DB 151 caatgaatgccccagaaatggcttcacatgccagccctaccacccaactgtaggtc 210
QY 63 TGAATCCCGATGGTACTACTGAAGTACGAGTCCGCCGGGTTATAGCGCCGCC 122
DB 211 tgaattcccatctggaaatatactgaacttgaatgcgcctcgttcttcggaaagac 270
QY 123 GTTTTATCATCTGCTGAAATACTGTCGTGAGTGGTGTAGAGACCGTGCAGC 182
DB 271 gtttctatcatctgcctaaataactcagctcgtactggtgtaaggacaggtgcagag 330
QY 183 TAAATCTGTGTATCCGCGAGATCCGTTAAGCATGGTGTGATGATCAAGCAT 242
DB 331 taatcaatgctgaatccctccagatccctggaatgcatgcatgcatcaaaagcat 390
QY 243 CCAAGTTGGTCCAAATTAATATCTGTACTAAAGTTACCGTCTGATGTTGTTCT 302
DB 391 ccaagttcgatcccaataataatctctgtactaaagataccgacatctgtctctc 450
QY 303 CAGCGTACATCATCTCTGTGATGATGATCTTGGATATGAACCGGATTTG 362

```

```

DB 451 gctgcacacgacatcatctccagtgatactctcatcttgggaataatgaacactattg 510
QY 363 TGACCGAATTCGGTGTGTCTGCGCGGACATCGCAACGGTATTTGACCTTATCAG 422
DB 511 tgaagaatctctgtggtgacaccccaacacaaatggaattcattagaccacaa 570
QY 423 TCGCGATATTTTACTATGATGTTCTGTGTGACCTACACATGCAATCTGAGTACCG 482
DB 571 cgaagagaatttcactatgatacagtgtagacctaaccgtgcaatcctggaagcgaag 630
QY 483 TAAAGGTGTGTAGCTGCGGCGGTGAGCGGCTCATCTGACATCAATACCAAGAGATCA 542
DB 631 ggaagaagtggttgagctgtggttgagccctccataatactgcacacgaatgagatca 690
QY 543 AATGGGATCTGGAGCGCGCGCGGACCGCATGTCATCATCCGAACAA 591
DB 691 agtggacatctgagcgccgcgcctcagtgcatatacctaacaacaa 739

```

RESULT 11

```

US-60-234-446-1627
: Sequence 1627, Application US/60234446
: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CL000832
: CURRENT APPLICATION NUMBER: US/60/234,446
: NUMBER OF SEQ ID NOS: 1797
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1627
: LENGTH: 574
: TYPE: DNA
: ORGANISM: HUMAN
US-60-234-446-1627

```

```

Query Match      73.0%; Score 431.2; DB 48; Length 574;
Best Local Similarity 84.6%; Pred. No. 8.2e-129;
Matches 464; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

```

```

QY 7 TGCACGCTCCGGAATGGCTGCTGCGCGCGGACCAACGATGATGATTTGAG 66
DB 2 tgaatgccccagaaatggcttcacatgccagccctaccacccaactgtaggtgag 61
QY 67 TTCCGATGGTACTACTGATGATGATGCGCGCGGTTATAGCGCGCGGTTT 126
DB 62 ttcccatggaacatcatctgaactatgaatgcatgcatgcatgcatgcatgcatgcat 121
QY 127 TGTATATGCTGCTGAAAACCTGCTGTGAGTGTGCTGAAGACCGTTGCCGATAAA 186
DB 122 tcatatattgtcttaaaactcagctcgtgcatggtgcatggaagaagtgagacgttaa 181
QY 187 TCTTGTGTAATCCGCGAGATCCGTTAAGCATGTCGATGATGATGATGATGATGAT 246
DB 182 tcatgtgtaacccctccagatccctggaatgcatgcatgcatgcatgcatgcatgcat 241
QY 247 TTGCGTCCCAATTAATATTTTGTGATGATGATGATGATGATGATGATGATGATGAT 306
DB 242 ttgsgatcccaataataatattctgtcctaaagataacgcatcattggttctcgtct 301
QY 307 GCTACATGATATATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 366
DB 302 gcaacatgatacatctcagtgatactgtcatttggataatagaacacccattatgtagc 361
QY 367 CGAATTCCTGTGATGCTGCGCGCGGACCGCATGCGGATGATGATGATGATGATGATGAT 426
DB 362 agaatctcctgtggtgcatcccccacatcaccaatgagattcattagacacaaga 421
QY 427 GATATTTTCACTATGATGTTCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 486

```


Tue Jan 16 09:11:51 2001

us-09-380-682-2.rmp

Page 10

```

1 GENERAL INFORMATION:
2 APPLICANT: Leshkowitz, Dena
3 APPLICANT: Liu, Jin
4 TITLE OF INVENTION: NOVEL CONFIGS OBTAINED FROM VARIOUS CDNA
5 FILE OF INVENTION: LIBRARIES
6 FILE REFERENCE: 20411-752CON1
7 CURRENT APPLICATION NUMBER: US/09/359, 922A
8 EARLIER FILING DATE: 1999-07-22
9 EARLIER APPLICATION NUMBER: US 09/205,155
10 EARLIER FILING DATE: 1998-12-03
11 EARLIER APPLICATION NUMBER: US 09/034,341
12 EARLIER FILING DATE: 1998-02-13
13 NUMBER OF SEQ ID NOS: 13203
14 SOFTWARE: FastSeq for Windows Version 3.0
15 SEQ ID NO 358
16 LENGTH: 6938
17 TYPE: DNA
18 ORGANISM: Homo sapiens
19 US-09-359-922-358

```

Query Match	68.8%;	Score 406.8;	DB 17;	Length 6938;
Best Local Similarity	83.8%;	Pred. No. 1.8e-120;		
Matches 496;	Conservative	0;	Mismatches 92;	Indels 4;
				Gaps 3

[illegible]

RESULT 15
US-09-716-475-3923

```

; Sequence 3923, Application US/09716475
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Vasicek, Thomas

```

```

1  TITLE OF INVENTION: NOVEL NOCLETIC ACID MOLECULES AND USES
2  TITLE OF INVENTION: THEREFOR
3  FILE REFERENCE: 1600.2037-001
4  CURRENT APPLICATION NUMBER: US/09/716,475
5  CURRENT FILING DATE: 2000-11-20
6  PRIOR APPLICATION NUMBER: 60/156,506
7  PRIOR FILING DATE: 1998-11-19
8  NUMBER OF SEQ ID NOS: 8194
9  SOFTWARE: FASTSEQ for Windows Version 4.0
10 SEQ ID NO 3923
11 LENGTH: 837
12 TYPE: DNA
13 ORGANISM: Homo sapiens
14 FEATURE:
15 NAME/KEY: misc.feature
16 LOCATION: (1) .. (837)
17 OTHER INFORMATION: n = A,T,C or G
18 US-09-716-475-3923

```

Query Match	45.88;	Score 270.4;	DB 24;	Length 837;
Best Local Similarity	85.58;	Pred. No. 1.4e-76;		
Matches 312; Conservative	0;	Mismatches 52;	Indels 1;	Gaps 1.

OY	4	CATGCGAAGCGCCGGATGGCTGCGCGTGGCGGCGCCGAGCAACGTGATCATTAATT	63
Db	138	caatgaataagccccagaatggtc-taattgcagcgctcaacaactaacctcigtgaattc	136
OY	64	GAGTTCGCAGTCGGTACCTACCTGAACATACGAATGCCGCCGGTTATAGCGGCCGCCG	123
Db	197	gaatttcccatctgggaacatactcgaactctgaattgacgcgccttgatctccggaagacg	256
OY	124	TTTTTCATCATCTGCCTGGAAAACTGTCTGTGATGGATGGTGTGAAGCAGCTTGCCGAGCT	183
Db	257	ttttcatcatctgctcaaaaaactcagctcgtgacgtggttgctaaagacagtgacagagt	316
OY	184	AAATCTGTGCGGAACCCGACGATCCGCGTTAACGCAATGCGGATGATGATCAAAAGCATC	243
Db	317	aaacacatgcgaaaccccgagaccgcggatgycatgagatgcatgcatgcaaaagacac	376
OY	244	CAGTTCGGTTCGCAATTAAATATCTTTACTATAAGGTACCGTGTGATGGTTCCTCC	303
Db	377	caattcggatcccaattaaatattctctgaataagatatccgactcattggttccctcg	436
OY	304	AGCGATACATCATCTCTGAGTATGTGATGTCATTTGGATATATAAACAACAGCATTTGT	363
Db	437	tcctgcacaatgatcatctcgtgatactgacatttggtgataatgaacacctatttgt	496
OY	364	GACCG 368	
Db	457	gacag 501	

Search completed: January 13, 2001, 13:41:06
Job time: 4081 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 12:32:20 ; Search time 85.47 Seconds
(Without alignments)
2597.597 Million cell updates/sec

Title: US-09-380-682-2
Sequence: 1 ATGCAGTGCACGCTCCGCA.....AGTGCATCATCCGACACAA 591

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq-36: *
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT: *
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT: *
3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT: *
4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT: *
5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT: *
6: /cgn2_2/gcgdata/geneseq/geneseqn/NA1985.DAT: *
7: /cgn2_2/gcgdata/geneseq/geneseqn/NA1986.DAT: *
8: /cgn2_2/gcgdata/geneseq/geneseqn/NA1987.DAT: *
9: /cgn2_2/gcgdata/geneseq/geneseqn/NA1988.DAT: *
10: /cgn2_2/gcgdata/geneseq/geneseqn/NA1989.DAT: *
11: /cgn2_2/gcgdata/geneseq/geneseqn/NA1990.DAT: *
12: /cgn2_2/gcgdata/geneseq/geneseqn/NA1991.DAT: *
13: /cgn2_2/gcgdata/geneseq/geneseqn/NA1992.DAT: *
14: /cgn2_2/gcgdata/geneseq/geneseqn/NA1993.DAT: *
15: /cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT: *
16: /cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT: *
17: /cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT: *
18: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT: *
19: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT: *
20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT: *
21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591	100.0	591	19	V53262 Complement recepto
2	583	98.6	591	19	V53273 Complement recepto
3	581.4	98.4	591	19	V53272 Complement recepto
4	579.8	98.1	591	19	V53270 Complement recepto
5	578.2	97.8	591	19	V53269 Complement recepto
6	573.4	97.0	591	19	V53271 Complement recepto
7	447.2	75.7	6951	10	N91477 CRI protein DNA.
8	447.2	75.7	6951	12	Q11642 Entire human comp
9	447.2	75.7	6951	20	Z38150 Human C3b/C4b rece
10	443.2	75.0	6951	14	Q41867 CRI coding region.
11	327.2	55.4	5420	12	Q11643 Partial human comp
12	327.2	55.4	5420	20	Z38151 Human C3b/C4b rece

13	225	38.1	228	19	V53279 Complement recepto
14	217	36.7	228	19	V53278 Complement recepto
15	215.4	36.4	228	19	V53277 Complement recepto
16	213.8	36.2	228	19	V53275 Complement recepto
17	212.2	35.9	228	19	V53274 Complement recepto
18	207.4	35.1	228	19	V53276 Complement recepto
19	63.4	10.7	3331	20	X84434 pB66-01, containi
20	61.2	10.4	74	19	V53285 Complement recepto
21	59.8	10.1	3327	12	Q10989 B lymphocyte membr
22	56	9.5	1365	18	T61098 DNA encoding porci
23	56	9.5	1365	20	Z09145 MCP cDNA. Unident
24	50	8.5	50	19	V53263 Complement recepto
25	47.8	8.1	125	19	X11827 Human diallelic po
26	47	8.0	47	19	V53264 Complement recepto
27	45.2	7.6	50	19	V53286 DAF protein coding
28	44.6	7.5	1146	20	V08935 Human tumour assoc
29	44.6	7.5	1493	20	X87915 Membrane co-factor
30	44.6	7.5	1878	17	T46065 Encodes human deca
31	44.6	7.5	2015	8	N70047 Human DAF cDNA. H
32	44.6	7.5	2096	16	Q99105 Human CD55 tumour
33	44.6	7.5	2096	18	T84471 Human CD55 tumour
34	44.6	7.5	2102	20	X87914 Decay accelerating
35	44.6	7.5	2115	10	N91043 Decay accelerating
36	44.6	7.5	2115	16	Q79863 Encodes human deca
37	44.6	7.5	2233	8	N70048 Membrane bound dec
38	44.6	7.5	2233	10	N91044 Decay accelerating
39	44.6	7.5	2233	16	Q79864 Human glycopospha
40	44.6	7.5	2237	18	T90287 CDA6 encoding a mo
41	43.4	7.3	2026	19	V09901 CDA6 construct sub
42	43	7.3	1134	17	T17598 Membrane cofactor
43	43	7.3	1134	17	T17596 rsmcp cDNA SEQ ID
44	38.2	6.5	756	14	Q46164
45	38.2	6.5	837	19	V40047

ALIGNMENTS

RESULT 1	
V53262	V53262 standard; DNA; 591 BP.
XX	
XX	V53262;
XX	18-JAN-1999 (first entry)
XX	
XX	Complement receptor type 1-like sequence CM7 DNA.
XX	
XX	Complement receptor type-1; CRI, CM7; complement; inhibitor;
KW	anti-haemolytic; multiple sclerosis; Parkinson's disease;
KW	xenograft rejection; inflammation; Crohn's disease; asthma;
KW	pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KW	autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KW	myasthenia gravis; reproductive disorder; therapy; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	W09839433-A1.
XX	
PD	11-SEP-1998.
XX	
XX	05-MAR-1998; 98WO-GB00727.
XX	
PR	05-MAR-1997; 97GB-0004519.
XX	
XX	(ADPR-) ADPROTECH PLC.
XX	
PI	Cox VF, Mossakowska DEI, Smith RAG;
XX	WPI: 1998-506358/43.
XX	P-PsDB; W79236.
DR	
XX	

PT Soluble polypeptide comprising short consensus repeats from LHR-A -
used to treat disorders and diseases associated with inflammation or
PT inappropriate complement activation
XX

PS Claim 22: Page 42-43; 67pp; English.

CC This DNA sequence encodes CM7 (see W9236), a protein that consists
CC of the short consensus repeats (SCR) 1 and 2 from the complement
CC receptor type 1 (CRI) fused to the SCR3 of CRI-like pseudogene (see
CC W9247). CM7 DNA was constructed using plasmid pDB1013-5, which
CC codes for SCR1-3 of CRI, by site-directed mutagenesis using 3 pairs
CC of oligonucleotides (see V53263-65) that introduced 10 amino acid
CC changes to the native SCR3 sequence corresponding to changes
CC observed in the CRI-like pseudogene (Cripse). pBROSCRI-3CM7
CC carrying the CM7 DNA construct was used to transform *Escherichia*
CC coli BL21(DE3), and CM7 was purified from solubilised inclusion
CC bodies. The invention provides DNA sequences (see V53262 and
CC V53269-79) encoding novel soluble engineered CRI polypeptides (see
CC W53236-47) such as CM7 that act as complement inhibitors with
CC functional complement inhibitory, including anti-haemolytic,
CC activity. These can be used to treat a disease or disorder
CC associated with inflammation or inappropriate complement activation,
CC such as neurological disorders (e.g. multiple sclerosis and
CC Parkinson's disease), disorders of inappropriate or undesirable
CC complement activation (e.g. xenograft rejection), inflammatory
CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),
CC post-ischaemic reperfusion conditions, infection or sepsis,
CC immune complex disorders and autoimmune diseases (e.g. rheumatoid
CC arthritis, proliferative nephritis and myasthenia gravis), and
CC reproductive disorders.
XX

Sequence 591 BP; 132 A; 159 C; 148 G; 152 T; 0 other;

Query Match 100.0%; Score 591; DB 19; Length 591;
Best Local Similarity 100.0%; Pred. No. 1,2e-190;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAATGCAACGCTCCGGAATGAGTGGCCGTCGCGCCGACCACTGATGATGA 60
DB 1 ATGCAATGCAACGCTCCGGAATGAGTGGCCGTCGCGCCGACCACTGATGATGA 60
QY 61 TTTGAGTCCCGATCGGATGATGATGATGATGATGATGATGATGATGATGATG 120
DB 61 TTTGAGTCCCGATCGGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 121 CCGTTTCTATCATCTGCTGAAACCTGCTGAGTGTGCTGAGACCGTTGCGGA 180
DB 121 CCGTTTCTATCATCTGCTGAAACCTGCTGAGTGTGCTGAGACCGTTGCGGA 180
QY 181 CGTAAATCTTGCGTAATCCGCGATGCGGTTAAGGATGATGATGATGATGATG 240
DB 181 CGTAAATCTTGCGTAATCCGCGATGCGGTTAAGGATGATGATGATGATGATG 240
QY 241 ATCCGATGCGTCCCAATTAATATCTTGTGATGATGATGATGATGATGATG 300
DB 241 ATCCGATGCGTCCCAATTAATATCTTGTGATGATGATGATGATGATGATG 300
QY 301 TCCAGCGTACATGATCATCTGATGATGATGATGATGATGATGATGATGATG 360
DB 301 TCCAGCGTACATGATCATCTGATGATGATGATGATGATGATGATGATGATG 360
QY 361 TGTGACCGGAATTCGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
DB 361 TGTGACCGGAATTCGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
QY 421 AGTCGGAGATTTTTCCTATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 421 AGTCGGAGATTTTTCCTATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 481 GGTAAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB 481 GGTAAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 540

QY 541 CAAGTGGGATCTGTGAGAGCGCCGCGACCGACGATGATGATGATGATGATG 591
DB 541 CAAGTGGGATCTGTGAGAGCGCCGCGACCGACGATGATGATGATGATGATG 591

RESULT 2

V53273
ID V53273 standard; DNA; 591 BP.

V53273;
AC

18-JAN-1999 (first entry)

DE Complement receptor type 1-like sequence CM6 DNA.

KM Complement receptor type-1; CRI; CM6; complement; inhibitor;

KM anti-haemolytic; multiple sclerosis; Parkinson's disease;

KM xenograft rejection; inflammation; Crohn's disease; asthma;

KM pancreatitis; post-ischaemic reperfusion; infection; sepsis;

KM autoimmune disease; rheumatoid arthritis; proliferative nephritis;

KM myasthenia gravis; reproductive disorder; therapy; ss.

OS Homo sapiens.

OS Synthetic.

PN W09893433-A1.

PD 11-SEP-1998.

PF 05-MAR-1998; 98WO-GB00727.

PR 05-MAR-1997; 97GB-0004519.

PA (ADPR-) ADPROTECH PLC.

PI Cox VF, Mossakowska DEI, Smith RAG;

PS Claim 22: Page 48; 67pp; English.

CC This DNA sequence encodes CM6 (see W9241), a protein that consists

CC of the short consensus repeats (SCR) 1 and 2 from complement

CC receptor type 1 (CRI) fused to an SCR3 (see W9246) in which 6 amino

CC acids were altered to those found in the SCR3 of the CRI-like

CC pseudogene (Cripse) putative product. CM6 DNA was constructed by

CC site-directed mutagenesis (see V53263 and V53265) of pDB1013-5, which

CC codes for SCR1-3 of CRI. pBROSCRI-3CM6 carrying CM6 DNA was used

CC to transform *Escherichia coli* BL21(DE3), and CM6 was purified from

CC solubilised inclusion bodies. The invention provides DNA sequences

CC (see V53262 and V53269-79) encoding novel soluble engineered CRI

CC polypeptides (see W53236-47) such as CM6 that act as complement

CC inhibitors with functional complement inhibitory, including

CC anti-haemolytic, activity. These can be used to treat a disease or

CC disorder associated with inflammation or inappropriate complement

CC activation, such as neurological disorders (e.g. multiple sclerosis

CC and Parkinson's disease), disorders of inappropriate or undesirable

CC complement activation (e.g. xenograft rejection), inflammatory,

CC post-ischaemic reperfusion conditions, infection or sepsis,

CC immune complex disorders and autoimmune diseases (e.g. rheumatoid

CC arthritis, proliferative nephritis and myasthenia gravis), and

CC reproductive disorders.
XX
SQ Sequence 591 BP; 135 A; 159 C; 146 G; 151 T; 0 other;

Query Match 98.6%; Score 583; DB 19; Length 591;
 Best Local Similarity 99.2%; Pred. No. 6e-188;
 Matches 586; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 1 ATGCAGTCAACGCTCCGGAATGGCTCCGTTCCGCCGCCGACCAACTGACTGATGAA 60
   |||||||
Db 1 atgcagtgcaacgctccggaaatggctccgttcgcgcgcgcgaacacccgactgataa 60
QY 61 TTTGAGTTCCTCGATCCGATACCTTACCTGATACGAAATGCGCCGGTTATAGCGCGC 120
   |||||||
Db 61 tttagagttccctcgatccgataccctgaactgaactgaatgcgcgggttataagcgcgc 120
QY 121 CCGTTTCTATCATCTGCTGAAAACTGTGTGAGCTGGTGTAGAGCCGTTGCGCA 180
   |||||||
Db 121 cgttttctatcatctgcgcgaataactcgtcgcgaactggtcctaagacgcgttcgca 180
QY 181 CGTAAATCTTGCTGTAATCCGCGAGATCCGATTACGCGATGATGATCAAAAGGC 240
   |||||||
Db 181 cgtaaactctgctgaatccgcagatccggttaacgcatggtgcatgatacaagc 240
QY 241 ATCCAGTTCGTTCCCAATTAATATCTTGTACTTAAAGTTACGTTGATTGTTCC 300
   |||||||
Db 241 atccagttcgtttcccaatlaaatacttctgaactaaagttaccgctcgtattgttcc 300
QY 301 TCCAGCGCTACATGATCATCTCTGATGATACGTATTTGGGATATGAACCGATT 360
   |||||||
Db 301 tccagcgctacatgatacatctctggtgatacgttcatcttgggataatgaacccgatt 360
QY 361 TGTAGCCGAATTCGCTGTGCTGCGCCGACCATCCCAACGGTGTACCTCATCTATC 420
   |||||||
Db 361 tgtagccgaatttcgctgtgctgcgcgcgacatcccaacgggtgttcatcttacc 420
QY 421 AGTCGCGAGTATTTTACTTACTTGTCTGTGTGATCACTACATGCAATCTGGTACCG 480
   |||||||
Db 421 aatcgcgagaatttctactatgtctgtgtgtaaccatactcgtggtgagcgt 480
QY 481 GGTAAAAAGGTGTTGAGCTCGTGGGAGCGGACCGTCACTACCTACATCAAAAGCAT 540
   |||||||
Db 481 ggtaaaaaggtgttgagctcgtggtgagcgcgtccatctactgactaagcaagacgat 540
QY 541 CAAATGGGATCTGAGAGCGGCCGCGACCGCATGATCAATCCGAAACAAA 591
   |||||||
Db 541 caaatgggactctgagagcgccgcacgcgagtgatcatcccgaaacaaa 591
  
```

RESULT 3
 V53272 standard; DNA; 591 BP.
 V53272;
 18-JAN-1999 (first entry)
 Complement receptor type 1-like sequence CMS DNA.
 Complement receptor type 1-like sequence CMS DNA.
 Complement receptor type-1; CRI; CMS; complement; inhibitor;
 anti-haemolytic; multiple sclerosis; Parkinson's disease;
 xenograft rejection; inflammation; Crohn's disease; asthma;
 pancreatitis; post-ischaemic reperfusion; infection; sepsis;
 autoimmune disease; rheumatoid arthritis; proliferative nephritis;
 myasthenia gravis; reproductive disorder; therapy; ss.
 Homo sapiens.
 Synthetic.
 WO9839433-A1.
 11-SEP-1998.
 05-MAR-1998; 98WO-GB00727.
 PF
 05-MAR-1997; 97GB-0004519.
 PR
 XX

(ADPR-) ADPROTECH PLC.
 XX Cox VE, Mossakowska DEI, Smith RAG;
 PI
 DR WPI; 1998-506358/43.
 XX P-PSDB; W79240.
 PT Soluble polypeptide comprising short consensus repeats from LHR-A -
 PT used to treat disorders and diseases associated with inflammation or
 PT inappropriate complement activation
 XX
 PS Claim 22; Page 47; 67pp; English.

This DNA sequence encodes CMS (see W79240), a protein that consists
 of the short consensus repeats (SCR) 1 and 2 from complement
 receptor type 1 (CRI) fused to an SCR3 (see W79245) in which 5 amino
 acids were altered to those found in the SCR3 of the CRI-like
 pseudogene (Cripse) putative product. CMS DNA was constructed by
 site-directed mutagenesis (see V53264-65) of pda103-5, which
 codes for SCR1-3 of CRI. ProSCR1-3CMS carrying CMS DNA was used
 to transform *Escherichia coli* BL21(DE3), and CMS was purified from
 the soluble inclusion bodies. The invention provides DNA sequences
 (see V53262 and V53269-79) encoding novel soluble engineered CRI
 polypeptides (see W53236-47) such as CMS that act as complement
 inhibitors with functional complement inhibitory, including
 anti-haemolytic, activity. These can be used to treat a disease or
 disorder associated with inflammation or inappropriate complement
 activation, such as neurological disorders (e.g. multiple sclerosis
 and Parkinson's disease), disorders of inappropriate or undesirable
 complement activation (e.g. xenograft rejection), inflammatory
 disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),
 post-ischaemic reperfusion conditions, infection or sepsis,
 immune complex disorders and autoimmune diseases (e.g. rheumatoid
 arthritis, proliferative nephritis and myasthenia gravis), and
 reproductive disorders.

Sequence 591 BP; 128 A; 160 C; 151 G; 152 T; 0 other:

Query Match 98.4%; Score 581.4; DB 19; Length 591;
 Best Local Similarity 99.0%; Pred. No. 2.1e-187;
 Matches 585; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 ATGCAGTCAACGCTCCGGAATGGCTCCGTTCCGCCGCCGACCAACTGACTGATGAA 60
   |||||||
Db 1 atgcagtgcaacgctccggaaatggctccgttcgcgcgcgcgaacacccgactgataa 60
QY 61 TTTGAGTTCCTCGATCCGATACCTTACCTGATACGAAATGCGCCGGTTATAGCGCGC 120
   |||||||
Db 61 tttagagttccctcgatccgataccctgaactgaactgaatgcgcgggttataagcgcgc 120
QY 121 CCGTTTCTATCATCTGCTGAAAACTGTGTGAGCTGGTGTAGAGCCGTTGCGCA 180
   |||||||
Db 121 cgttttctatcatctgcgcgaataactcgtcgcgaactggtcctaagacgcgttcgca 180
QY 181 CGTAAATCTTGCTGTAATCCGCGAGATCCGATTACGCGATGATGATCAAAAGGC 240
   |||||||
Db 181 cgtaaactctgctgaatccgcagatccggttaacgcatggtgcatgatacaagc 240
QY 241 ATCCAGTTCGTTCCCAATTAATATCTTGTACTTAAAGTTACGTTGATTGTTCC 300
   |||||||
Db 241 atccagttcgtttcccaatlaaatacttctgaactaaagttaccgctcgtattgttcc 300
QY 301 TCCAGCGCTACATGATCATCTCTGATGATACGTATTTGGGATATGAACCGATT 360
   |||||||
Db 301 tccagcgctacatgatacatctctggtgatacgttcatcttgggataatgaacccgatt 360
QY 361 TGTAGCCGAATTCGCTGTGCTGCGCCGACCATCCCAACGGTGTACCTCATCTATC 420
   |||||||
Db 361 tgtagccgaatttcgctgtgctgcgcgcgacatcccaacgggtgttcatcttacc 420
QY 421 AGTCGCGAGTATTTTACTTACTTGTCTGTGTGATCACTACATGCAATCTGGTACCG 480
   |||||||
  
```

Db 421 agtcgcagatatttcacatagttctgtgtacctaaccgtgcgaatccggtagcgt 480
QY 481 GGTAAAGAGGTTTGAGCTGTGTGGTGGAGCGCTCCATCTACTGACAGAAAGAGAT 540
||| |||||
Db 481 ggtcgttaagggttttgagctcgttggtagcggtccatctactgtacacgaagaagat 540
QY 541 CAAGTGGCATCTGGAGCGCGCCGACCGCAGCTGCATATCCGACAA 591
|||||
Db 541 caagtggcatcttgagcgccgcagcgacgtgcatactccgaacaa 591
RESULT 4
V53270
ID V53270 standard; DNA: 591 BP.
XX V53270;
AC V53270;
XX
DT 18-JAN-1999 (first entry)
DE Complement receptor type 1-like sequence CM2 DNA.
XX
KM Complement receptor type-1; CRI; CM2; complement; inhibitor;
KM anti-hemolytic; multiple sclerosis; Parkinson's disease;
KM xenograft rejection; inflammation; Crohn's disease; asthma;
KM pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KM autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KM myasthenia gravis; reproductive disorder; therapy; ss.
XX
OS Homo sapiens.
XX Synthetic.
XX WO9839433-A1.
PN 11-SEP-1998.
PD 05-MAR-1998; 98WO-GB00727.
PE 05-MAR-1998; 98WO-GB00727.
XX
PR 05-MAR-1997; 97GB-0004519.
XX
PA (ADPR-) ADPROTECH PLC.
XX
PI Cox VF, Mossakowska DEL, Smith RMG;
XX WPI: 1998-506358/43.
DR P-PSDB; W/9238.
XX
PT Soluble polypeptide comprising short consensus repeats from LHR-A -
PT used to treat disorders and diseases associated with inflammation or
PT inappropriate complement activation
XX
PS Claim 22: Page 45: 67pp: English.
XX
CC This DNA sequence encodes CM2 (see W/9238), a protein that consists
CC of the short consensus repeats (SCR) 1 and 2 from complement
CC receptor type 1 (CRI) fused to an SCR3 (see W/9243) in which 4 amino
CC acids were altered to those found in the SCR3 of the CRI-like
CC pseudogene (CR1pse) putative product. CM2 DNA was constructed by
CC site-directed mutagenesis (see V53264) of plasmid pDB1013-5, which
CC codes for SCR1-3 of CRI. pProcCRI-3CM2 carrying CM2 DNA was used
CC to transform Escherichia coli BL21(DB3), and CM2 was purified from
CC solidified inclusion bodies. The invention provides DNA sequences
CC (see V53262 and V53269-79) encoding novel soluble engineered CRI
CC polypeptides (see W53236-47) such as CM2 that act as complement
CC inhibitors with functional complement inhibitory, including
CC anti-hemolytic, activity. These can be used to treat a disease or
CC disorder associated with inflammation or inappropriate complement
CC activation, such as neurological disorders (e.g. multiple sclerosis
CC and Parkinson's disease), disorders of inappropriate or undesirable
CC complement activation (e.g. xenograft rejection), inflammatory
CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),
CC post-ischaemic reperfusion conditions, infection or sepsis,
CC immune complex disorders and autoimmune diseases (e.g. rheumatoid
CC arthritis, proliferative nephritis and myasthenia gravis), and

CC reproductive disorders.
XX
SQ Sequence 591 BP; 134 A; 158 C; 146 G; 153 T; 0 other:
Query Match 98.1%; Score 579.8; DB 19; Length 591;
Best Local Similarity 98.8%; Pred. No. 7.3e-187;
Matches 584; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 ATGCAGTGCAGACGCTCCGGAATGAGCTGCGCTTCGCGCGCCGACCACTGATGATGAA 60
|||
Db 1 atgcagtgcaacgctccggaatgagctgctgcgcgcgcacccaactgacatgaa 60
QY 61 TTGAGTTCGCCATGAGGAGCTTACCTGAATAGATGCGCGCGGTTATGAGCGCGC 120
|||
Db 61 ttgagttcccgatcgcgaactgacactgaaactgaaatgacgcgcggttataagcgccgc 120
QY 121 CCGTTTCTATCATCTGCTGTAAGAAACTCTGTCTGAGCTAGTCTTAAGACCGTTGCCGA 180
|||
Db 121 ccgtttccatacatctgcctgaaactctgtcgaactgacgtgctaaaggaccgttgcga 180
QY 181 CGTAAATCTGTCTGAATCCGCGATCCGTTAACGGCATGTCATGATCAAGAGC 240
|||
Db 181 cgtaaatctgtcgttaatccgcgcagatccggttaacgcatgtgcatgtataaaggc 240
QY 241 ATCCAGTTGCGTCCCAATTAATATATCTGTGACTGATTAAGGTTACCGTGTGATGCTTC 300
|||
Db 241 atccagttcggtcccaatataatattctgtactaaagggttaacgctgtatgtcttc 300
QY 301 TCCAGCGCTACATGATATATCTGCTGATACGTGATTTGGGATTAAGAACCCGATT 360
|||
Db 301 tcacgcgcaacatgacatcatctcgtgaaacgcatcatcttggaataagaaacccgalt 360
QY 361 TGTGACCGAATTCGTTGCTGTCGCGCGACCATGCGCAAGGATTTCCATCTATTC 420
|||
Db 361 tgtgacccaatctcgttgcgttcgctgcgcgcacatcaacaaggatctcatccacc 420
QY 421 AGTCGCGAGTATTTCACTATGATGTTGTGTGATGACCTACGCAATCGGTGAGCGGT 480
|||
Db 421 aatcgcgagaattttcaactatgattcgtgtgtagactaacatctgtgtagcgcgt 480
QY 481 GGTAAAGAGGTTTGAGCTGTGTGGTGGAGCGCTCCATCTACTGACAGAAAGAGAT 540
|||
Db 481 ggttaaaagggtttgagctcgttggtagcggtccatctactgtacacgaagaagat 540
QY 541 CAAGTGGCATCTGGAGCGCGCCGACCGCAGTGCATATCCGACAA 591
|||||
Db 541 caagtggcatcttgagcgccgcagcgacgtgcatactccgaacaa 591
RESULT 5
V53269
ID V53269 standard; DNA: 591 BP.
XX V53269;
AC V53269;
XX
DT 18-JAN-1999 (first entry)
DE Complement receptor type 1-like sequence CM1 DNA.
XX
KM Complement receptor type-1; CRI; CM1; complement; inhibitor;
KM anti-haemolytic; multiple sclerosis; Parkinson's disease;
KM xenograft rejection; inflammation; Crohn's disease; asthma;
KM pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KM autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KM myasthenia gravis; reproductive disorder; therapy; ss.
XX
OS Homo sapiens.
XX Synthetic.
XX WO9839433-A1.
PN 11-SEP-1998.

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XX PF 05-MAR-1998; 98MO-GB00727.
XX PR 05-MAR-1997; 97GB-0004519.
XX PA (ADPR-) ADPROTECH PLC.
XX PI Cox VF, Mossakowska DEI, Smith RAG;
XX DR WPI: 1998-506358/43.
XX DR P-PSDB; W79237.
XX PT Soluble polypeptide comprising short consensus repeats from LHR-A -
XX PR used to treat disorders and diseases associated with inflammation or
XX PT inappropriate complement activation
XX PS Claim 22; Page 44; 67pp; English.
XX CC This DNA sequence encodes CM1 (see W79237), a protein that consists
XX CC of the short consensus repeats (SCR) 1 and 2 from complement
XX CC receptor type 1 (CRI) fused to an SCR3 (see W79242) in which 5 amino
XX CC acids were altered to those found in the SCR3 of the CRI-1-like
XX CC pseudogene (Cripse) putative product. CM1 DNA was constructed by
XX CC site-directed mutagenesis (see V53263) of plasmid pDB1013-5, which
XX CC codes for SCR1-3 of CRI. pBrosCRI-3CM1 carrying CM1 DNA was used
XX CC to transform Escherichia coli BL21(DE3), and CM1 was purified from
XX CC solubilised inclusion bodies. The invention provides DNA sequences
XX CC (see V53262 and V53269-79) encoding novel soluble engineered CRI
XX CC polypeptides (see W53236-47) such as CM1 that act as complement
XX CC inhibitors with functional complement inhibitory, including
XX CC anti-hemolytic, activity. These can be used to treat a disease or
XX CC disorder associated with inflammation or inappropriate complement
XX CC activation, such as neurological disorders (e.g. multiple sclerosis
XX CC and Parkinson's disease), disorders of inappropriate or undesirable
XX CC complement activation (e.g. xenograft rejection), inflammatory
XX CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),
XX CC post-ischaemic reperfusion conditions, infection or sepsis,
XX CC immune complex disorders and autoimmune diseases (e.g. rheumatoid
XX CC arthritis, proliferative nephritis and myasthenia gravis), and
XX CC reproductive disorders.
SQ Sequence 591 BP; 127 A; 159 C; 151 G; 154 T; 0 other;

Query Match 97.8%; Score 578.2; DB 19; Length 591;
Best Local Similarity 98.6%; Pred. No. 2.5e-186;
Matches 583; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 ATGCAGTGCAGCGCCGGAATGGCGCGCGCGCCGACACCACTGATATGA 60
DB 1 atgcagtcgaacgcctccggaatcgcctgcgcgcgcgcacccaactgactgtatga 60
OY 61 TTGAGTTCGCCGATGCGTACTACCTAGACTAGCAATGCCGCCGGGTATAGCGCC 120
DB 61 ttgagttccgccgatgctgactactcgaactcgaatgcgcgcgggtatatagcgccgc 120
OY 121 CCGTTTCTATATCTGCTGAAACCTGTCTGTGACTGTGCTTAAGGACCGTTGCC 180
DB 121 cggtttctatctgctgctgaaacctgtctgtgactgtgctttaaggaccgttgcga 180
OY 181 CGTAATATCTGTCGTAATCCGACAGTCCGTTACGCGATGGTGATGTGATCAAGGC 240
DB 181 cgtaatatctgtcgtaatccgacagatccggttaagcagatggtgataatcaaggc 240
OY 241 ATCCAGTTCGTTCCCAATTAATTTCTGTACTAAGAGTTACCGTGTGATGGTTC 300
DB 241 atccagttcgtttcccaattaatcttctgtactaagagttaccgttattgttcc 300
OY 301 TCCAGCGCTACATGCATCTCTGTGTACTGCTGATCTATTGGATATGAACACCGAT 360
DB 301 tccagcgctacatgcatactctctgtgtactgctgatactattggatataaacacgatt 360
OY 361 TGTGACCGAATTCGGTGTGCTGCGCGGACCAATGGCAAGGATTTCACTCTATC 420

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DB 361 tgtgacccaattccgtgtgtctgcgcgcgcacaccacgcgaagtgatctccctcacc 420
OY 421 AGTCGCGAGTATTTTCACTATGTTCTGTGTGATGACCTACCACTGCAATCTGGTAGCCGT 480
DB 421 agtcgcgagatcttccactatgttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
OY 481 GGTAAAAAGGTTTGTGAGCTGCTGGGTAGCCGCTCCATCTACTGCACTAAGCAACGAT 540
DB 481 ggtcgaagggttgtgagctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
OY 541 CAAGTGGGCATCTGAGCGCGCCGACCGCAGTGCATCATCCGAAACAA 591
DB 541 caagtgggcattctgagcgcgcgcgcacgcagtgatcatcatccgaacaa 591

RESULT 6
V53271
ID V53271 standard; DNA: 591 BP.
XX AC V53271;
XX XX
DT 18-JAN-1999 (first entry)
XX XX
DE Complement receptor type 1-like sequence CM3 DNA.
XX XX
KW Complement receptor type-1; CRI; CM3; complement; inhibitor;
KW anti-hemolytic; multiple sclerosis; Parkinson's disease;
KW xenograft rejection; inflammation; Crohn's disease; asthma;
KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KW myasthenia gravis; reproductive disorder; therapy; ss.
XX XX
OS Homo sapiens.
OS Synthetic.
OS W09839433-A1.
XX PD 11-SEP-1998.
XX PF 05-MAR-1998; 98MO-GB00727.
XX PR 05-MAR-1997; 97GB-0004519.
XX PA (ADPR-) ADPROTECH PLC.
XX PI Cox VF, Mossakowska DEI, Smith RAG;
XX DR WPI: 1998-506358/43.
XX DR P-PSDB; W79239.
XX PT Soluble polypeptide comprising short consensus repeats from LHR-A -
XX PR used to treat disorders and diseases associated with inflammation or
XX PT inappropriate complement activation
XX PS Claim 22; Page 46; 67pp; English.
XX CC This DNA sequence encodes CM2 (see W79239), a protein that consists
XX CC of the short consensus repeats (SCR) 1 and 2 from complement
XX CC receptor type 1 (CRI) fused to an SCR3 (see W79244) in which 1 amino
XX CC acid was altered to that found in the SCR3 of the CRI-1-like
XX CC pseudogene (Cripse) putative product. CM3 DNA was constructed by
XX CC site-directed mutagenesis (see V53265) of plasmid pDB1013-5, which
XX CC codes for SCR1-3 of CRI. pBrosCRI-3CM3 carrying CM3 DNA was used
XX CC to transform Escherichia coli BL21(DE3), and CM3 was purified from
XX CC solubilised inclusion bodies. The invention provides DNA sequences
XX CC (see V53262 and V53269-79) encoding novel soluble engineered CRI
XX CC polypeptides (see W53236-47) such as CM3 that act as complement
XX CC inhibitors with functional complement inhibitory, including
XX CC anti-hemolytic, activity. These can be used to treat a disease or
XX CC disorder associated with inflammation or inappropriate complement
XX CC activation, such as neurological disorders (e.g. multiple sclerosis
XX CC and Parkinson's disease), disorders of inappropriate or undesirable

```


Db	571	agagagaatttccactctatgctcagtcgtggtgaccctcagcgtcgaatcctctgaaagcgaggg	630
Oy	484	AAAAAGGTGTTTGAGCTCGTGGGTGAGCCGTGCATCTACTGCTAGCAAGAGATCAA	543
Db	631	agaagaagtgttctgagctctgtggtgagagccctcatatctgacacagcaatgacgtcaa	690
Oy	544	GTGGGCACTCTGGAGCGGCCCGGACACCGCATGCTCATCCGGAACAA	591
Db	691	gtggagcatcttgagagcgccccccctcagtcattatatactaaacaa	738
RESULT	8		
ID	Q11642	standard; DNA: 6951 BP.	
XX	Q11642;		
XX	25-JUN-1991	(first entry)	
XX		Entire human complement type 1 receptor coding region.	
XX		complement system; C3b/C4b receptor; CRI; allergic reaction;	
XX		immune response; clone lambda T109.1; ss.	
OS		Homo sapiens.	
XX	Key	Location/Qualifiers	
XX	sig_peptide	28..147	
XX		/*tag= a	
XX		/note= "putative"	
XX	mat_peptide	148..6144	
XX		/*tag= b	
XX		/product= C3b/C4b receptor	
XX	WO9105047-A.		
XX	18-APR-1991.		
XX	25-SEP-1990;	90WO-US05454.	
XX	26-SEP-1989;	89US-0412745.	
XX	26-SEP-1990;	90US-0912349.	
XX		(TCEL-) T CELLS SCI INC.	
XX		(UYJO) JOHNS HOPKINS UNIVERSITY.	
XX		(BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.	
XX		Fearon DT, Klickestein LB, Wong WW, Carson GR, Hoh M, Concino MF,	
XX		Makrides SC, Marsh HC;	
XX		WP1: 1991-132854/18.	
XX		P-PSDB; R1810.	
XX		Human complement receptor type 1 gene, encoded proteins and	
XX		fragments - for treatment of immune disorders, myocardial infarct,	
XX		damage due to inflammation and in treatment of thrombosis	
PS	Claim 1; Fig 1; 234pp; English.		
XX		This sequence is a composite of sequences isolated as lambda clones	
XX		RI10.3, T109.1, H3.1 and H7.1. The clones were present in the	
XX		specifically primed lambda gIII cDNA library (Lambda HH) which was	
XX		prepared with cDNA synthesised from poly(A)+ RNA from DMSO induced	
XX		HL-60 cells. The library was screened using probes CRI-1, CR-2 and	
XX		CR1-4 (see Wong, WW et al., 1985, Proc. Nat. Acad. Sci. USA, 82:7711)	
XX		and probe CRI-18 (corresponding to nucleotides 101-352 of this	
XX		sequence). There are four direct, long homologous repeats of 450bp,	
XX		each comprising 7 short consensus repeats. Nucleotides 28-1533 are	
XX		also claimed separately.	
XX		See also Q11643.	
XX		Sequence 6951 BP: 1802 A; 1681 C; 1659 G; 1809 T; 0 other:	

[illegible]

CC may be mediated through the inhibition of complement pathway enzymes. The soluble CRI protein exhibits a complement regulatory activity, and this CC may be used to prevent reperfusion injury, inhibit Arhus reaction, and CC neutrophil mediated tissue damage, and reduce myocardial infarct size, CC and inflammation. The CRI protein and its fragments can also be used in CC the treatment of conditions which involve unwanted complement activity, e.g. shock lung, tissue damage due to burn, or ischemic heart conditions, CC and autoimmune disorders. CRI proteins, analogues, derivatives, and anti-CRI antibodies are used in assays, and diagnostics. The present sequence CC represents a fragment of the gene encoding the human CRI protein.
xx

S0 Sequence 5420 BP; 1435 A; 1295 C; 1263 G; 1427 T; 0 other;

Query Match 55.48; Score 327.2; DB 20; Length 5420;
Best Local Similarity 72.3%; Pred. No. I.le-100;
Matches 425; Conservative 0; Mismatches 163; Indels 0; Gaps 0

Y 4 CATGTCAACGATCCGGAGTGCCTGCCGTGGCGCCCGACAACCTGATGATATT 63
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1320 cactgtcaacgccccagatcatcttctcgttgccaaagtgaacaaccatacatcct 1379

Gy 64 GAATTCGCCAATCGTACTACCTGAACACTACGAAATCCGCCCGGGTTATGAGCGCCGCC 123
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1380 gaatttcgccaatcggtacctttaagaatgaagcgcgtccctcagactaacaggagaagca 1439

	Query Match	55.4%	Score 327.2;	DB 20;	Length 5420;
	Best Local Similarity	72.3%;	Pred. No. 1.1e-100;		
	Matches	425;	Conservative	0;	Mismatches 163; Indels 0; Gaps 0
Oy	4	CAGTGCACGCTCCGGAAATGCGTCGCCGTTCGCGGCCCGACCAACTGACTGATGAATT	63		
Db	1320	cacttgcgaagccccagatcattcttcgtttgccaagtvgaaacccaaccaatgcatct	1379		
Oy	64	GACTTCCGATCGGACCTACTCGAAGTACGATGCCGCCGGTTATAGCCAGCCCCC	123		
Db	1380	gaattcccatctggacacctttaagaatgacatgcgctccctgatactaaggagagca	1459		
Oy	124	TTTTCATANTCGCTCGAAAACCTGTCGTGACATGCTGTAAAGACCGTTGCCGAGT	183		
Db	1440	tctctcatacaatgctcagataaccctgycctgvtcaagatcccaagaagtctctgttaaacgt	1499		

Db 1500 aaatcatgtcaaaacccctcccgatcccgatgaagcgcattggtgcacatgaacacac 155
QY 244 CAGTCGGTTCGCAATTAAATATTCCTTGACCTAAGGATTACCGCTCATGTGGTCTCC 303

QY 304 AGCGCTACATGTCATCTCTGGTGATCTGTCTATTGGGAATAGAAACACCGATTTC 365
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1620 tctctcgatgtatcctcttcaggaacatctgcgcatcttggaagcaagccggcaatttgc 1679

364 GACCGAATTCGGTGTGCTGCGCGCGACCATCGCCAACGGTGATTTCACCTCTATCAGT 423

Db 1680 caacgaattcctgtggtaccccccaaccatcgccaatgagatttcattagcaccac 173

424 CGCGAGTATTTTCACTATGGTCTGTGGTGACCTACCACCTGCATCTGGGTAGCCGGT 483

Db 1740 agagagaattttcactatgatcagtggtgacctaccgctgcaatcttgaagcagagg 179

484 AAAAAGGTGTTGAGCTCGTGGGTGAGCCGTCATCTACTGCAC TAGCAAAGACGATCAA 543

Db 1800 agaaagtggttgagctgtggtgagccctcatactgcaaccagcaatgacgatcaa 185

544 GTGGCATCTGGAGCGGCCCGCACCAGTGCATCATCCGACAA 591

Db 1860 gtggcatctgagcggcccccagtgcatatactaaca 1907

V53279

[illegible]

16/12/64

[illegible]

complement receptor type 1-like sequence cmt2b cmt2b

anti-haemolytic: multiple sclerosis; Parkinson's disease; complement receptor type-1; CRI; CMI4; complement; inhibitor; KW

KW xenograft rejection; inflammation; Crohn's disease; ascluna;
KW pancreatitis: post-ischaemic reperfusion: infection: sepsis:

Db	64	gagaatttcactaagctctgctctgctgaactacacacgcatctcgtgtagccgtgtgaaa	123
QY	487	AAGGTATTTGACATCGTGGGTGAGCCGCTGCATCTACGCACTGCAAGAGCATCAAGTG	546
Db	124	aaggtattttgaaactcgtgtgtgtgtagccgtgcacatcactgcgactctgcaaaagcagcatcaagt	183
QY	547	GGCATCTGGAGCGCCGCGCAACGAGTGCATCATCCGAAACAA	591
Db	184	ggagatcttgagcgcgcgcgcgcacgcgaatgagctatctcccgaaacaa	228

RESULT 15

V5321	
ID	V53277 standard; DNA; 228 BP.
XX	

AC V53277

DT 18-JAN-1999 (first entry)
YYDE Complement receptor type 1-like sequence CML2 DNA
VY

KM Complement receptor type-1; CRI; CMI2; complement; inhibitor;
KM anti-haemolytic; multiple sclerosis; Parkinson's disease;
KM xenograft rejection; inflammation; Crohn's disease; asthma;
KM paracellitis; post-ischemic reperfusion; infection; sepsis;
KM autoimmune disease; rheumatoid arthritis; proliferative nephritis
KM myasthenia gravis; reproductive disorder; therapy; ss.

OS Homo sapiens.
OS Synthetic.

PN WO9839433-A1.

PD 11-SEP-1998
XX

PE 05-MAR-1998; 98WO-GB00727.
XY

PR 05-MAR-1997; 97GB-0004519.
XX

PA (ADPR-) ADPROTECH PLC.
XX

PI Cox VE, Mossakowska DEI, Smith RAG;
VV

DR WPI; 1998-506358/43.
DB P-BEND; W70745

DR P-PSDB; W79245.

PT Soluble polypeptide comprising short consensus repeats from LHR-A -
PT used to treat disorders and diseases associated with inflammation or
PT inappropriate complement activation

PS Claim 22; Page 50; 67pp; English.

CC This DNA sequence encodes CM12 (see W792445), a protein that consists
CC of the short consensus repeat 3 (SCR3) of complement receptor type
CC 1 (CR1) in which 5 amino acid residues have been substituted by
CC the amino acids theoretically encoded by CR1-like pseudogene
CC CR1pse. This SCR3 is also found in polypeptide CM5 (see W792400).
CC Plasmid pPROSCRL3-CM12 carrying CM12 DNA was used to transform
CC *Escherichia coli* BL21(DE3), and CM12 was purified from solidified
CC inclusion bodies. The invention provides DNA sequences (see V53262
CC and V53269-79) encoding the novel soluble engineered CR1 polypeptides
CC (see W53265-47) such as CM12 that act as complement inhibitors with
CC functional complement inhibitory, including anti-haemolytic,
CC activity. These can be used to treat a disease or disorder
CC associated with inflammation or inappropriate complement activation
CC such as neurological disorders (e.g. multiple sclerosis and
CC Parkinson's disease), disorders of inappropriate or undesirable
CC complement activation (e.g. xenograft rejection), inflammatory
CC disorders (e.g. Crohn's disease, asthma and acute pancreatitis),
CC post-ischaemic reperfusion conditions, infection or sepsis,
CC immune complex disorders and autoimmune diseases (e.g. Rheumatoid
CC arthritis, proliferative nephritis and myasthenia gravis), and

CC reproductive disorders.
XX
SQ Sequence 228 BP; 46 A; 63 C; 65 G; 54 T; 0 other;

Query Match	36.4%;	Score 215.4;	DB 19;	Length 228;
Best Local Similarity	97.3%;	Pred. No. 1.9e-63;		
Matches 219; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

OY	367	CGAATTCGCGGAGGTCGTGCGCGCCACCATCGCCAGGAGATTACCTCATCAATGTCG	426
Db	4	cgaattccgctgtgtcgtcgcgcgcgaaccatcgccaagaagtgattcaactctatacgtcgc	63
OY	427	GAGTATTTTCACTATGTTGTTCTGTGTGTGTGTAACCTACCACTGCATCTGGGTAGCCGTGTGTA	486
Db	64	ggaattttcaactatgattctgtctgtgtgtaacctaacgctgtgcaatccggtgtagtcgtgt	123
OY	487	AAGGTGTTTBAAGCTCGTGGGTGAGCGCGTCCATCTACTGCACATGCAAAAGAGATCAAGTG	546
Db	124	aaggtgtttttagatcgtctgtgtgttagtcgcgttcacatctactgactgacaagaagatcaatg	183
OY	547	GGCATCTGGAGCGCCCGGCCAACCGAGTGCATCATCCCGAACAA	591
Db	184	ggcatctggagcgcgcgcgcgcacgcgcatgtgcatcatctcccgatacaa	228

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 12:30:50 ; Search time 65.7 Seconds
(without alignments)
1449.707 Million cell updates/sec

Title: US-09-380-682-2

Sequence: 1 ATGCAGTGCACACGCTCCGGA.....AGTGCATCATCCGACACAA 591

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 segs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, NA:*

- 1: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/lna/6_COMB.seq:*
- 4: /cgn2_6/ptodata/2/lna/PCITUS_COMB.seq:*
- 5: /cgn2_6/ptodata/2/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558.2	94.5	605	2	US-08-769-967A-33
2	447.2	75.7	6951	5	5256642-1
3	447.2	75.7	6951	5	5472939-1
4	327.2	55.4	5420	5	5256642-3
5	327.2	55.4	5420	5	5472939-3
6	204.2	34.6	243	2	US-08-769-967A-32
7	101	17.1	101	2	US-08-356-361-3
8	101	17.1	101	2	US-08-356-361-4
9	101	17.1	101	2	US-08-356-361-5
10	101	17.1	101	2	US-08-356-361-6
11	101	17.1	101	2	US-08-769-967A-3
12	101	17.1	101	2	US-08-769-967A-4
13	101	17.1	101	2	US-08-769-967A-5
14	101	17.1	101	2	US-08-769-967A-6
15	93	15.7	93	2	US-08-356-361-2
16	93	15.7	93	2	US-08-769-967A-2
17	86.4	14.6	94	2	US-08-356-361-7
18	86.4	14.6	94	2	US-08-769-967A-7
19	86	14.6	87	2	US-08-356-361-1
20	86	14.6	87	2	US-08-769-967A-1
21	78.4	13.3	90	2	US-08-356-361-8
22	78.4	13.3	90	2	US-08-769-967A-8
23	75.4	12.8	85	2	US-08-356-361-11
24	75.4	12.8	85	2	US-08-356-361-12
25	75.4	12.8	85	2	US-08-769-967A-11
26	75.4	12.8	85	2	US-08-769-967A-12
27	68.8	11.6	79	2	US-08-356-361-13
28	68.8	11.6	79	2	US-08-769-967A-13

C 29	68	11.5	78	2	US-08-356-361-10	Sequence 10, Appl
C 30	68	11.5	78	2	US-08-769-967A-10	Sequence 10, Appl
C 31	61.8	10.5	81	2	US-08-356-361-21	Sequence 21, Appl
C 32	61.8	10.5	81	2	US-08-769-967A-21	Sequence 21, Appl
C 33	60.8	10.3	75	2	US-08-356-361-14	Sequence 14, Appl
C 34	60.8	10.3	75	2	US-08-769-967A-14	Sequence 14, Appl
C 35	60	10.2	72	2	US-08-356-361-9	Sequence 9, Appl
C 36	60	10.2	72	2	US-08-769-967A-9	Sequence 9, Appl
C 37	58.4	9.9	85	2	US-08-356-361-22	Sequence 22, Appl
C 38	58.4	9.9	85	2	US-08-769-967A-22	Sequence 22, Appl
C 39	44.6	7.5	860	1	US-08-310-416A-19	Sequence 19, Appl
C 40	44.6	7.5	860	1	US-08-888-171-19	Sequence 19, Appl
C 41	44.6	7.5	969	1	US-08-310-416A-12	Sequence 12, Appl
C 42	44.6	7.5	969	1	US-08-888-171-12	Sequence 12, Appl
C 43	44.6	7.5	1134	3	US-08-793-418-14	Sequence 4, Appl
C 44	44.6	7.5	1878	2	US-08-435-149-17	Sequence 17, Appl
C 45	44.6	7.5	2096	1	US-08-458-084-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-769-967A-33
; Sequence 33, Application US/08769967A
; Patent No. 5859223
; GENERAL INFORMATION:
; APPLICANT: Mossakowska, Danuta E.I.
; APPLICANT: Smith, Richard A.G.
; APPLICANT: Dodd, Ian
; APPLICANT: Freeman, Anne Mary
; TITLE OF INVENTION: Soluble CRI Derivatives
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporate Intellectual Property
; STREET: P.O. Box 1539
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,967A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/440,569
; FILING DATE: 15-May-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: P30423C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5364
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-769-967A-33
Query Match 94.5% Score 558.2; DB 2; Length 605;
Best Local Similarity 97.6% Pred. No. 1.8e-178;
Matches 577; Conservative 0; Mismatches 13; Indels 1; Gaps 1;


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Db 211 gagttcccatgaggacatactgaactatgaatgcgcgccttgattccaggaaagccg 270
Qy 124 TTTTCTATCATCTGCCTGAAAAAAGCTGTCTGTGACTGTGTCTAAGAACCGTTCGCAAGT 183
Db 271 ttctcatcatcgtcctaanaaacctcagctcgtgctgaagcaggtgcagagcgt 330
Qy 184 AATATCTTGCTGTAATCCGGCAGATCCGGTTAAAGGCATGTGTGATGTGATCAAGGCATC 243
Db 331 aaatcatcgtcctaatactccacagatccctgtaagcagatggtcagctgacaaagcagtc 390
Qy 244 CAGTTGGTTCCTCCAAATTAATATTTCTTGTACTTAAAGTTAGCTGATGGTTCCTCC 303
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Qy 304 AGCGTACATGCATCATCTCTGTGTACTGTCTGATTTGGGTAATGAACACCGATTGTG 363
Db 451 tctgcacatcgtcctacatccaaagtgtactgtcattgtggaataatgaacacatttgt 510
Qy 364 GACCGAATTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 423
Db 511 gacagaaattcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 570
Qy 424 CCGGATATTTTCTACTATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 483
Db 571 agagagaatttctacatcgtatcagtggtgacactaccgctgcacatcctggaagcgaggg 630
Qy 484 AAAAAGCTTTGAGCTCGTGGGTGAGCGCTGCATCTACTGTGACAGTAAAGACGATCAA 543
Db 631 agaaaggtgttgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 690
Qy 544 GTGGGATCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 591
Db 691 gtgggcatctgagagcgcgccgcgcctcagtgcatcatalactaacaa 738

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RESULT 4
5256642-3
; Patent No. 5256642
; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LOYD B.; WONG,
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
; TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
; RECEPTOR 1 (CR1) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
; USE THEREOF
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,128
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 412,745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332,865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176,532
; FILING DATE: 01-APR-1988
; SEQ ID NO: 3
; LENGTH: 5420
5256642-3

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Query Match 55.4%; Score 327.2; DB 5; Length 5420;
Best Local Similarity 72.3%; Pred. No. 3.2e-100;
Matches 425; Conservative 0; Mismatches 163; Indels 0; Gaps 0;
Qy 4 CAGTGAACGCTCCGGAATGCTGCGCTTGCAGCGCCGACGACCACTGACTGATGATT 63
Db 1320 cactgcaagcccccaataatcttctgttgcgaagtgtgaaacccaacaaatgatct 1379
Qy 64 GAGTTCCTCCGATCGTACTGAACTGAACCTGAATGCCGCCGGGTTATAGCGGCCCGC 123
Db 1380 gacttcccatgagacatcttaagtaagaaatgcgcctcgtgactactacggagcgca 1439

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Qy 124 TTTTCTATCATCTGCCTGAAAAAAGCTGTCTGTGACTGTGTCTAAGAACCGTTCGCAAGT 183
Db 1440 ttctcatcaatcgtctagatacactgctgtcgtcgaagctcccaagaatgtctgtaaagct 1499
Qy 184 AATATCTTGCTGTAATCCGGCAGATCCGGTTAAAGGCATGTGTGATGTGATCAAGGCATC 243
Db 1500 aaatcatcgtcctaatactccacagatccctgtaagcagatggtcagctgacaaagcagtc 1559
Qy 244 CAGTTGGTTCCTCCAAATTAATATTTCTTGTACTTAAAGTTAGCTGATGGTTCCTCC 303
Db 1560 cagttcgtggtcccaataataatctctgtaccaaagcagcagctcatctgttcaactca 1619
Qy 304 AGCGTACATGCATCATCTCTGTGTACTGTCTGATTTGGGTAATGAACACCGATTGTG 363
Db 1620 tctgcgaatgtactcctcagaactacgtcccatctggaagcagagcgccaatttgt 1679
Qy 364 GACCGAATTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 423
Db 1680 caagaaattcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1739
Qy 424 CCGGATATTTTCTACTATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 483
Db 1740 agagagaatttctacatcgtatcagtggtgacactaccgctgcacatcttgaagcagaggg 1799
Qy 484 AAAAAGCTTTGAGCTCGTGGGTGAGCGCTGCATCTACTGTGACAGTAAAGACGATCAA 543
Db 1800 agaaaggtgttgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1859
Qy 544 GTGGGATCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 591
Db 1860 gtgggcatctgagagcgcgccgcgcctcagtgcatcatalactaacaa 1907

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RESULT 5
5472939-3
; Patent No. 5472939
; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LOYD B.; WONG,
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
; TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
; MEDIATED DISORDERS
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138,825
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 588,128
; FILING DATE: 24-SEP-1990
; APPLICATION NUMBER: 412,745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332,865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176,532
; FILING DATE: 01-APR-1988
; SEQ ID NO: 3
; LENGTH: 5420
5472939-3

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Query Match 55.4%; Score 327.2; DB 5; Length 5420;
Best Local Similarity 72.3%; Pred. No. 3.2e-100;
Matches 425; Conservative 0; Mismatches 163; Indels 0; Gaps 0;
Qy 4 CAGTGAACGCTCCGGAATGCTGCGCTTGCAGCGCCGACGACCACTGACTGATGATT 63
Db 1320 cactgcaagcccccaataatcttctgttgcgaagtgtgaaacccaacaaatgatct 1379
Qy 64 GAGTTCCTCCGATCGTACTGAACTGAACCTGAATGCCGCCGGGTTATAGCGGCCCGC 123
Db 1380 gacttcccatgagacatcttaagtaagaaatgcgcctcgtgactactacggagcgca 1439
Qy 124 TTTTCTATCATCTGCCTGAAAAAAGCTGTCTGTGACTGTGTCTAAGAACCGTTCGCAAGT 183

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Db 1440 ttctctacatgctcagataaccgctgctgctcaagtcaccaagatgctctaaagct 1499
QY 184 AAATCTGTGATTCGGCCAGATCCGGTTACGGCATGCTGATGATCAAGCATC 243
Db 1500 aaatcgaataaactcccaagatccagatgatacgtgctgctgatacagaacac 1559
QY 244 CAGTGGTGTCCCAATTAATATCTGTACTAAGGTTACCGTGTGTTGCTCTCC 303
Db 1560 caggttgatccagaatcaactatctctgtaatacagggccagcattggtcactca 1619
QY 304 AGCCCTCATGATCATCTCTGTGTACTGTCTATTGAGTAATGAACAACGATTTG 363
Db 1620 tctgtcgaatgtaactcctcagcaatactgctcattgagcagaagccgcaattgt 1679
QY 364 GACGGAATTCGGTGTGCTGCGCGGACCATCGCAAGGTGATTCACCTCATCAGT 423
Db 1680 caacgaatcctctggtggtccaccccaacacacgcacatggaatctcattagcacaac 1739
QY 424 CGCGATATTTTCACTATGCTGTGTGACTACCACTGCAATCTGGGTAGCCGTGGT 483
Db 1740 agagaatcttcaactatgatacagtgtaacctacgcgtcaactctggaagcagaag 1799
QY 484 AAAAGGTGTTGAGTCTGCTGCTGAGCCGTCATCTGCTGCTGCTGCTGCTGCTGCT 543
Db 1800 agaaagtgcttgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1859
QY 544 GTGGGCAATCTGGAGCGCGCGGACCGCATGATCATCCGGAACAA 591
Db 1860 gtgggcaatctggagcgcgccgctcagtgatcattacctaaca 1907

RESULT 6
US-08-769-967A-32
Sequence 32, Application US/08769967A
Patent No. 5859223
GENERAL INFORMATION:
APPLICANT: Mossakowska, Danuta E.I.
APPLICANT: Smith, Richard A.G.
APPLICANT: Dodd, Ian
APPLICANT: Freeman, Anne Mary
TITLE OF INVENTION: Soluble CRI Derivatives
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporate Intellectual Property
STREET: P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,967A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 08/440,569
FILING DATE: 15-May-1995
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: P30423C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5364
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

POPOLOGY: linear
MOLECULE TYPE: DNA
US-08-769-967A-32
Query Match 34.6%; Score 204.2; DB 2; Length 243;
Best Local Similarity 94.2%; Pred. No. 1.7e-59;
Matches 212; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 367 CGAATTCGTTGCTGTGCTGCGGACCATCGCAAGGTGATTCACCTCATCAGTCG 426
Db 7 CGAATTCGTTGCTGTGCTGCGGACCATCGCAAGGTGATTCACCTCATCAGTCG 66
QY 427 GAGTATTTTCACTATGCTGTGTGAGCTACCACTGATCATCTGGGTAGCCGTGGT 486
Db 67 GAGTATTTTCACTATGCTGTGTGAGCTACCACTGATCATCTGGGTAGCCGTGGT 126
QY 487 AAGGTGTTGAGCTGCTGCTGAGCCGCTCATCTACTGCACTAGCAAGATCAAGTG 546
Db 127 AAGGTGTTGAGCTGCTGCTGAGCCGCTCATCTACTGCACTAGCAAGATCAAGTG 186
QY 547 GGCATCTGAGCGCGCGGACCGCATGATCATCCGGAACAA 591
Db 187 GGCATCTGAGCGCGCGGACCGCATGATCATCCGGAACAA 231

RESULT 7
US-08-356-361-3
Sequence 3, Application US/08356361
Patent No. 5833989
GENERAL INFORMATION:
APPLICANT: Smith, Richard A.G.
APPLICANT: Dodd, Ian
APPLICANT: Freeman Mary A.
APPLICANT: Mossakowska, Danuta E.I.
TITLE OF INVENTION: No. 5833989el Compounds
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham-corporate Intellectual Property
STREET: P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,361
FILING DATE: 03-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P30423
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-356-361-3

Query Match 17.1%; Score 101; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 GAACAGATGCGCGCGCGGTTATACGCGCGCGCGGTTTCTATCATCTGCTGAAAA 146
DB 1 GAACAGATGCGCGCGCGGTTATACGCGCGCGCGGTTTCTATCATCTGCTGAAAA 60
QY 147 CTCTGCTGAGTGTGCTAGGACGCTGCGCGAGTAAT 187
DB 61 CTCTGCTGAGTGTGCTAGGACGCTGCGCGAGTAAT 101

RESULT 8

US-08-356-361-4/C
; Sequence 4, Application US/08356361
; Patent No. 5833989
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard A.G.
; APPLICANT: Dodd, Ian
; APPLICANT: Freeman Mary A.
; APPLICANT: Mossakowska, Danuta E.I.
; TITLE OF INVENTION: No. 5833989el Compounds
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham-Corporate Intellectual Property
; STREET: P.O. Box 1539
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,361
; FILING DATE: 03-Jul-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jervis, Herbert H.
; REGISTRATION NUMBER: 31,171
; REFERENCE/DOCKET NUMBER: P30423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5019
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-356-361-4

Query Match 17.1%; Score 101; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 AATGCCCGCGGTTATAGCGCGCGGTTTCTATCATCTGCTGAAAAAAGTCTGCT 154
DB 101 AATGCCCGCGGTTATAGCGCGCGGTTTCTATCATCTGCTGAAAAAAGTCTGCT 42
QY 155 GACCTGCTGTAAGACCGTTGCCGAGTAATCTGCTG 195
DB 41 GACCTGCTGTAAGACCGTTGCCGAGTAATCTGCTG 1

RESULT 9

US-08-356-361-5
; Sequence 5, Application US/08356361
; Patent No. 5833989
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard A.G.

APPLICANT: Dodd, Ian
APPLICANT: Freeman Mary A.
APPLICANT: Mossakowska, Danuta E.I.
TITLE OF INVENTION: No. 5833989el Compounds
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham-Corporate Intellectual Property
STREET: P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,361
FILING DATE: 03-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P30423
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-356-361-5

Query Match 17.1%; Score 101; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 CTCTGCTATCCGCCGAGATCCGCTTACGCGATGCTGATCAAGCATCCAGT 247
DB 1 CTCTGCTATCCGCCGAGATCCGCTTACGCGATGCTGATCAAGCATCCAGT 60
QY 248 TCGGTTCCCAATTAATATTCTGTACTAAGGTTACGT 288
DB 61 TCGGTTCCCAATTAATATTCTGTACTAAGGTTACGT 101

RESULT 10

US-08-356-361-6/C
; Sequence 6, Application US/08356361
; Patent No. 5833989
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard A.G.
; APPLICANT: Dodd, Ian
; APPLICANT: Freeman Mary A.
; APPLICANT: Mossakowska, Danuta E.I.
; TITLE OF INVENTION: No. 5833989el Compounds
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham-Corporate Intellectual Property
; STREET: P.O. Box 1539
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,361
; FILING DATE: 03-Jul-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jervis, Herbert H.
; REGISTRATION NUMBER: 31,171
; REFERENCE/DOCKET NUMBER: P30423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5019
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-356-361-6

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,361
FILING DATE: 03-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P30423
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-356-361-6

Query Match 17.1%; Score 101; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 AATCGGCGATCGGTTACGGCATGTGATCAAGAGCATCGATTGGTTC 285
DB 101 AATCGGCGATCGGTTACGGCATGTGATCAAGAGCATCGATTGGTTC 42
OY 256 CAATTAATTTCTTCTACTAAGGTTCACCGTCTGATTGG 296
DB 41 CAATTAATTTCTTCTACTAAGGTTCACCGTCTGATTGG 1

RESULT 11
US-08-769-967A-3
Sequence 3, Application US/08769967A
Patent No. 5859223
GENERAL INFORMATION:
APPLICANT: Mossakowska, Danuta E.I.
APPLICANT: Smith, Richard A.G.
APPLICANT: Dodd, Ian
APPLICANT: Freeman, Anne Mary
TITLE OF INVENTION: Soluble CRI Derivatives
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithline Beecham Corporate Intellectual Property
STREET: P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,967A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/440,569
FILING DATE: 15-May-1995
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: P30423C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5364
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 101 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-769-967A-3

Query Match 17.1%; Score 101; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 GAATCGATGCGCGCGGTTATACGGCGCGCGGTTTCTATCATCTCGTAATAA 146
DB 1 GAATCGATGCGCGCGGTTATACGGCGCGCGGTTTCTATCATCTCGTAATAA 60
OY 147 CTCTGTGACTGTGCTAAGACGCTTCCGACGTAAT 187
DB 61 CTCTGTGACTGTGCTAAGACGCTTCCGACGTAAT 101

RESULT 12
US-08-769-967A-4/C
Sequence 4, Application US/08769967A
Patent No. 5859223
GENERAL INFORMATION:
APPLICANT: Mossakowska, Danuta E.I.
APPLICANT: Smith, Richard A.G.
APPLICANT: Dodd, Ian
APPLICANT: Freeman, Anne Mary
TITLE OF INVENTION: Soluble CRI Derivatives
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithline Beecham Corporate Intellectual Property
STREET: P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,967A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/440,569
FILING DATE: 15-May-1995
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: P30423C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5364
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-769-967A-4

Query Match 17.1%; Score 101; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,361
FILING DATE: 03-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jervils, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P30423
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-356-361-2

Query Match 15.7%; Score 93; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 TGCAGTGCACGCTCCGAGATGCTGCCGCGCCGCGACCAACTGACTGATGAAT 61
Db 93 TGCAGTGCACGCTCCGAGATGCTGCCGCGCCGCGACCAACTGACTGATGAAT 61
OY 62 TTGAGTCCCGATCGGTACTACTGAACTACG 94
Db 33 TTGAGTCCCGATCGGTACTACTGAACTACG 1

Search completed: January 13, 2001, 13:10:27
Job time: 2377 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 12:28:05 ; Search time 1135.8 Seconds

(without alignments)
2662.960 Million cell updates/sec

Title: US-09-380-682-2

Perfect score: 591
Sequence: 1 ATGCAGTCACACGCTCCGGA.....AGTCATCATCCCGACACAA 591

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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21: em_pat: *
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23: em_pl: *
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25: em_sts: *
26: em_sy: *
27: em_un: *
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30: gb_in1: *
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32: gb_in3: *
33: gb_pl3: *
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37: em_htg1: *
38: em_htg2: *
39: em_htg3: *
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41: em_htg5: *
42: em_htg6: *
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44: em_htg8: *
45: em_htg9: *
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48: em_hum4: *
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79: gb_pi33: *
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81: gb_pi35: *
82: gb_pi36: *
83: em_htg0: *
84: gb_pi37: *
85: gb_pi38: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591	100.0	591	81	A86593 Sequence 2
2	583	98.6	591	81	A86609 Sequence 18
3	581.4	98.4	591	81	A86607 Sequence 16
4	579.8	98.1	591	81	A86603 Sequence 10
5	578.2	97.8	591	81	A86601 Sequence 12
6	573.4	97.0	591	81	A86605 Sequence 14
7	558.2	94.5	605	81	AR029199 Sequence
8	447.2	75.7	2376	53	HSCRIHS
9	447.2	75.7	2376	53	G28591
10	447.2	75.7	6951	57	HSCRI
11	445.6	75.4	1985	51	CHPCRIWT
12	445.6	75.4	6044	51	CHPCRIWT
13	416.8	70.5	1688	51	BARCORE
14	406.4	68.8	945	51	BARCOREA
15	404.6	68.5	1731	51	CHPCRI
16	399.2	67.5	6000	53	BARCRIA
17	327.2	55.4	5420	53	HSCRI
18	261.6	44.3	1680	11	D42115
19	261.6	44.3	1724	11	R45112
20	261.6	44.3	1811	11	R45112
21	254.4	43.0	1781	11	MUSCRL

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22 236.2 40.0 1272 11 MOSCR2AB
23 234.2 39.6 2102 11 MOSCR2AB
24 225 38.1 228 81 A86619
25 217 36.7 228 81 A86619
26 215.4 36.4 228 81 A86619
27 213.8 36.2 228 81 A86619
28 212.2 35.1 228 81 A86619
29 207.4 35.1 228 81 A86619
30 204.2 34.6 223 81 A86619
31 183.8 31.1 990 11 MOSXG
32 174.4 29.5 389 77 G25967
33 174.4 29.5 389 77 G27827
34 173.8 29.4 309 85 HUMCPLA
35 168.2 28.5 591 85 HUMCR15F12
36 168 28.4 433 85 HUMCR15
37 168 28.4 170965 72 HUMCR15F25
38 166.2 28.1 666 85 HUMCR15F25
39 166.2 28.1 187065 73 HUMCR15F25
40 165.4 28.0 744 85 HUMCR15F19
41 163.2 27.6 187065 73 HUMCR15F19
42 161 27.2 750 85 HUMCR15F05
43 153.4 26.0 1527 11 GPCR15
44 146.2 24.7 1272 11 D42116
45 135.2 22.9 268 11 R42CR1X
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ALIGNMENTS

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RESULT 1
LOCUS A86593
DEFINITION Sequence 2 from Patent WO9839433.
ACCESSION A86593
VERSION A86593.1 GI:6735168
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Smith, R.A. and Cox, V.F.
TITLE COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
JOURNAL Patent: WO 9839433-A 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
FEATURES
Source 1..591
Location/Qualifiers
BASE COUNT 132 a 159 c 148 g 152 t
ORIGIN
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Query Match 100.0%; Score 591; DB 81; Length 591;
Best Local Similarity 100.0%; Pred. No. 7.1e-175;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGCAGTGCACAGCTCCGGAATGAGTGCCTTGCAGCCGCCGACCAACCTGACTGATGAA 60
DB 1 ATGCAGTGCACAGCTCCGGAATGAGTGCCTTGCAGCCGCCGACCAACCTGACTGATGAA 60
QY 61 TTGAGTCCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCC 120
DB 61 TTGAGTCCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCC 120
QY 121 CCGTTTCTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 CCGTTTCTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 CGTAAATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 CGTAAATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ATCCAGTTCGGTTCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
DB 241 ATCCAGTTCGGTTCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
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DB 241 ATCCAGTTCGGTTCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
QY 301 TCCAGGCTACATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 TCCAGGCTACATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 TGTGACCGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 TGTGACCGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AGTCGGAGTATTTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 AGTCGGAGTATTTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 GGTAAAGGTTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 540
DB 481 GGTAAAGGTTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 540
QY 541 CAAGTGGCATCTGGAGGCGCCGCGACCGGACGATGATCCCGAACA 591
DB 541 CAAGTGGCATCTGGAGGCGCCGCGACCGGACGATGATCCCGAACA 591
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RESULT 2
LOCUS A86609
DEFINITION Sequence 18 from Patent WO9839433.
ACCESSION A86609
VERSION A86609.1 GI:6735179
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Smith, R.A. and Cox, V.F.
TITLE COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
JOURNAL Patent: WO 9839433-A 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
FEATURES
Source 1..591
Location/Qualifiers
BASE COUNT 135 a 159 c 146 g 151 t
ORIGIN
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Query Match 98.6%; Score 583; DB 81; Length 591;
Best Local Similarity 99.2%; Pred. No. 2.3e-172;
Matches 586; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 1 ATGCAGTGCACAGCTCCGGAATGAGTGCCTTGCAGCCGCCGACCAACCTGACTGATGAA 60
DB 1 ATGCAGTGCACAGCTCCGGAATGAGTGCCTTGCAGCCGCCGACCAACCTGACTGATGAA 60
QY 61 TTGAGTCCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCC 120
DB 61 TTGAGTCCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCC 120
QY 121 CCGTTTCTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 CCGTTTCTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 CGTAAATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 CGTAAATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ATCCAGTTCGGTTCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
DB 241 ATCCAGTTCGGTTCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
QY 301 TCCAGGCTACATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 TCCAGGCTACATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
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Db 301 TCACGGGCTACATGCATCATCTCTGGTGAATCTGATTTGGGATAATGAACCGGATT 360
QY 361 TGTGACCGAATTCCTGCTGTGCTGCGCGGACCATCGCAACGGTGAATTTACCTCTATC 420
Db 361 TGTGACCGAATTCCTGCTGTGCTGCGCGGACCATCGCAACGGTGAATTTACCTCTATC 420
QY 421 AGTCGGAGATTTTACATGATGTTCTGTGTGATGCTTACCACTGCAATCTGGGTACCGT 480
Db 421 AGTCGGAGATTTTACATGATGTTCTGTGTGATGCTTACCACTGCAATCTGGGTACCGT 480
QY 481 GGTAAAAAGGTGTTTGAAGCTGCGGTGAGCCGCTCCATCTACTGCACTAGCAAGACGAT 540
Db 481 GGTAAAAAGGTGTTTGAAGCTGCGGTGAGCCGCTCCATCTACTGCACTAGCAAGACGAT 540
QY 541 CAAGTGGCATCTGGAGCGCGCCGCGACCGACGACATGATCCGGAACAA 591
Db 541 CAAGTGGCATCTGGAGCGCGCCGCGACCGACGACATGATCCGGAACAA 591
RESULT 3
AB6607 591 bp DNA PAT 21-JAN-2000
LOCUS AB6607
DEFINITION Sequence 16 from Patent WO9839433.
ACCESSION AB6607
VERSION AB6607.1 GI:6735178
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 591)
AUTHORS Smith, R.A. and Cox, V.F.
TITLE COMPLEMENT RECEPTOR TYPE 1 (CRI)-LIKE SEQUENCES
JOURNAL Patent: WO 9839433-A 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
FEATURES
source 1..591
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 128 a 160 c 151 g 152 t
ORIGIN
Query Match 98.4%; Score 581.4; DB 81; Length 591;
Best Local Similarity 99.0%; Pred. No. 7.4e-172;
Matches 585; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 421 AGTCGGAGATTTTACATGATGTTCTGTGTGATGCTTACCACTGCAATCTGGGTACCGT 480
Db 421 AGTCGGAGATTTTACATGATGTTCTGTGTGATGCTTACCACTGCAATCTGGGTACCGT 480
QY 481 GGTAAAAAGGTGTTTGAAGCTGCGGTGAGCCGCTCCATCTACTGCACTAGCAAGACGAT 540
Db 481 GGTAAAAAGGTGTTTGAAGCTGCGGTGAGCCGCTCCATCTACTGCACTAGCAAGACGAT 540
QY 541 CAAGTGGCATCTGGAGCGCGCCGCGACCGACGACATGATCCGGAACAA 591
Db 541 CAAGTGGCATCTGGAGCGCGCCGCGACCGACGACATGATCCGGAACAA 591
RESULT 4
AB6603 591 bp DNA PAT 21-JAN-2000
LOCUS AB6603
DEFINITION Sequence 12 from Patent WO9839433.
ACCESSION AB6603
VERSION AB6603.1 GI:6735176
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 591)
AUTHORS Smith, R.A. and Cox, V.F.
TITLE COMPLEMENT RECEPTOR TYPE 1 (CRI)-LIKE SEQUENCES
JOURNAL Patent: WO 9839433-A 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
FEATURES
source 1..591
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 134 a 158 c 146 g 153 t
ORIGIN
Query Match 98.1%; Score 579.8; DB 81; Length 591;
Best Local Similarity 98.8%; Pred. No. 2.4e-171;
Matches 584; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

481 GGTAAAGAGTGTGAGCTGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
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Db 481 GGTAAAGAGTGTGAGCTGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
QY 541 CAAGTGGGATCTGGAGCGCCCGGACCGCATGATCCGGAACAA 591
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Db 541 CAAGTGGGATCTGGAGCGCCCGGACCGCATGATCCGGAACAA 591
RESULT 5
A86601 591 bp DNA PAT 21-JAN-2000
LOCUS A86601 Sequence 10 from Patent WO9839433.
DEFINITION A86601
ACCESSION A86601 GI:6735175
VERSION
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Smith, R.A. and Cox, V.F.
TITLE COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
JOURNAL Patent: WO 9839433-A 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
FEATURES
source 1..591
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 127 a 159 c 151 g 154 t
ORIGIN

Query Match 97.8%; Score 578.2; DB 81; Length 591;
Best Local Similarity 98.6%; Pred. No. 7.6e-172;
Matches 363; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ATGCAGTGCACGCTCGGAAATGAGCTGCGCGCGCCGACCAACCTGATGATGAA 60
Db 1 ATGCAGTGCACGCTCGGAAATGAGCTGCGCGCGCCGACCAACCTGATGATGAA 60
QY 61 TTGAGTTCCTCGATCGTACCTACCTAGCAATGCGCGCGGTTATAGCGGCGC 120
Db 61 TTGAGTTCCTCGATCGTACCTACCTAGCAATGCGCGCGGTTATAGCGGCGC 120
QY 121 CGGTTTCTATCATCTGCTGTAAGAACTCTGCTGAGAGTGGTAAAGACCGTGGCGA 180
Db 121 CGGTTTCTATCATCTGCTGTAAGAACTCTGCTGAGAGTGGTAAAGACCGTGGCGA 180
QY 121 CGGTTTCTATCATCTGCTGTAAGAACTCTGCTGAGAGTGGTAAAGACCGTGGCGA 180
Db 121 CGGTTTCTATCATCTGCTGTAAGAACTCTGCTGAGAGTGGTAAAGACCGTGGCGA 180
QY 181 CGTAATCTGTCGTAATCCGCGAGATCCGTTACGCGAGTGCATGTGATCAAAAGC 240
Db 181 CGTAATCTGTCGTAATCCGCGAGATCCGTTACGCGAGTGCATGTGATCAAAAGC 240
QY 241 ATCCAGTTCGCTCCAAATTAATATCTGTAAGAGTTACCGTCTGATGGTTC 300
Db 241 ATCCAGTTCGCTCCAAATTAATATCTGTAAGAGTTACCGTCTGATGGTTC 300
QY 301 TCCAGCGCTACATCATCTCTGATGATCTGATTTGGATTAATGAACACCGATT 360
Db 301 TCCAGCGCTACATCATCTCTGATGATCTGATTTGGATTAATGAACACCGATT 360
QY 361 TGTAGCGCAATTCGATGATCTCTGATGATCTGATTTGGATTAATGAACACCGATT 420
Db 361 TGTAGCGCAATTCGATGATCTCTGATGATCTGATTTGGATTAATGAACACCGATT 420
QY 421 AGTCGCGAGTATTTTCACTATGTTCTGTGGTGACCTACCATCGAATCTGGAGCGGT 480
Db 421 AGTCGCGAGTATTTTCACTATGTTCTGTGGTGACCTACCATCGAATCTGGAGCGGT 480
QY 481 GGTAAAGAGTGTGAGCTGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
Db 481 GGTAAAGAGTGTGAGCTGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
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541 CAAGTGGGATCTGGAGCGCCCGGACCGCATGATCCGGAACAA 591
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Db 541 CAAGTGGGATCTGGAGCGCCCGGACCGCATGATCCGGAACAA 591
RESULT 6
A86605 591 bp DNA PAT 21-JAN-2000
LOCUS A86605 Sequence 14 from Patent WO9839433.
DEFINITION A86605
ACCESSION A86605
VERSION A86605.1 GI:6735177
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Smith, R.A. and Cox, V.F.
TITLE COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
JOURNAL Patent: WO 9839433-A 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
FEATURES
source 1..591
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 131 a 160 c 149 g 151 t
ORIGIN

Query Match 97.0%; Score 573.4; DB 81; Length 591;
Best Local Similarity 98.1%; Pred. No. 2.5e-169;
Matches 580; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGCAGTGCACGCTCGGAAATGAGCTGCGCGCGCCGACCAACCTGATGATGAA 60
Db 1 ATGCAGTGCACGCTCGGAAATGAGCTGCGCGCGCCGACCAACCTGATGATGAA 60
QY 61 TTGAGTTCCTCGATCGTACCTACCTAGCAATGCGCGCGGTTATAGCGGCGC 120
Db 61 TTGAGTTCCTCGATCGTACCTACCTAGCAATGCGCGCGGTTATAGCGGCGC 120
QY 121 CGGTTTCTATCATCTGCTGTAAGAACTCTGCTGAGAGTGGTAAAGACCGTGGCGA 180
Db 121 CGGTTTCTATCATCTGCTGTAAGAACTCTGCTGAGAGTGGTAAAGACCGTGGCGA 180
QY 121 CGGTTTCTATCATCTGCTGTAAGAACTCTGCTGAGAGTGGTAAAGACCGTGGCGA 180
Db 121 CGGTTTCTATCATCTGCTGTAAGAACTCTGCTGAGAGTGGTAAAGACCGTGGCGA 180
QY 181 CGTAATCTGTCGTAATCCGCGAGATCCGTTACGCGAGTGCATGTGATCAAAAGC 240
Db 181 CGTAATCTGTCGTAATCCGCGAGATCCGTTACGCGAGTGCATGTGATCAAAAGC 240
QY 241 ATCCAGTTCGCTCCAAATTAATATCTGTAAGAGTTACCGTCTGATGGTTC 300
Db 241 ATCCAGTTCGCTCCAAATTAATATCTGTAAGAGTTACCGTCTGATGGTTC 300
QY 301 TCCAGCGCTACATCATCTCTGATGATCTGATTTGGATTAATGAACACCGATT 360
Db 301 TCCAGCGCTACATCATCTCTGATGATCTGATTTGGATTAATGAACACCGATT 360
QY 361 TGTAGCGCAATTCGATGATCTCTGATGATCTGATTTGGATTAATGAACACCGATT 420
Db 361 TGTAGCGCAATTCGATGATCTCTGATGATCTGATTTGGATTAATGAACACCGATT 420
QY 421 AGTCGCGAGTATTTTCACTATGTTCTGTGGTGACCTACCATCGAATCTGGAGCGGT 480
Db 421 AGTCGCGAGTATTTTCACTATGTTCTGTGGTGACCTACCATCGAATCTGGAGCGGT 480
QY 481 GGTAAAGAGTGTGAGCTGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
Db 481 GGTAAAGAGTGTGAGCTGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
QY 541 CAAGTGGGATCTGGAGCGCCCGGACCGCATGATCCGGAACAA 591
Db 541 CAAGTGGGATCTGGAGCGCCCGGACCGCATGATCCGGAACAA 591
RESULT 7

LOCUS	AR029199	605 bp	DNA	PAT	29-SEP-1999
DEFINITION	Sequence	33	from patent US 5859223.		
ACCESSION	AR029199				
VERSION	AR029199.1	GI:5941172			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 605)				
AUTHORS	Mossakowska, D., Ewalirena, D., I., Freeman, A., Mary, and Smith, R. Anthonygodwin.				
TITLE	Soluble CRL derivatives				
JOURNAL	Patent: US 5859223-A 33 12-JAN-1999;				
FEATURES	Location/Qualifiers				
source	1..605				
BASE COUNT	136 a	161 c	150 g	158 t	
ORIGIN	/organism="unknown"				
Query Match	94.5%;	Score 558.2;	DB 81;	Length 605;	
Best Local Similarity	97.6%;	Pred. No. 1.5e-164;			
Matches	577;	Conservative	0;	Mismatches 13;	Indels 1;
					Gaps 1;
OY	1	ATGCAGTCAACGCTCCGGATGSGTGCCTGCGCGCCCGACCACTGACTGATGAA	60		
Db	4	ATGCAGTCAACGCTCCGGATGSGTGCCTGCGCGCCCGACCACTGACTGATGAA	63		
OY	61	TTTGATGCCGATGGTGAACCTGTAACCTGTAACCTGTAACCTGTAACCTGTAAC	120		
Db	64	TTTGATGCCGATGGTGAACCTGTAACCTGTAACCTGTAACCTGTAACCTGTAAC	123		
OY	121	CCGTTTCTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180		
Db	124	CCGTTTCTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	183		
OY	181	CGTAATCTTGTGCTGAATCCGCGCAGATCCGCTGTAACGGGATGGTGCATGTGATCA	240		
Db	184	CGTAATCTTGTGCTGAATCCGCGCAGATCCGCTGTAACGGGATGGTGCATGTGATCA	243		
OY	241	ATCCAGTTCGGTTCCTCCCAATTAATATCTCTTACTAAAGTTACCGTGTGTTGCC	300		
Db	244	ATCCAGTTCGGTTCCTCCCAATTAATATCTCTTACTAAAGTTACCGTGTGTTGCC	303		
OY	301	TCCAGCGCTACATGCATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360		
Db	304	TCCAGCGCTACATGCATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	363		
OY	361	TGTGACCGAATTCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	420		
Db	364	TGTGACCGAATTCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	423		
OY	421	AGTCGCGAGTATTTTCACTAGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	480		
Db	424	AATCCCGAGAAATTTTCACTAGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	483		
OY	481	GCTAAAGGTTGAGCTGCTGGGTGAGCCGCTCATCTACTGCACTGCAAAAGCAT	540		
Db	484	GCTAAAGGTTGAGCTGCTGGGTGAGCCGCTCATCTACTGCACTGCAAAAGCAT	543		
OY	541	CAAGTGGGATCTGAGAGGCGCCGCGACCGACGATGCATCATCCGAAACAA	591		
Db	544	CAAGTGGGATCTGAGAGGCGCCGCGACCGACGATGCATCATCCGAAACAA	593		
RESULT	8				
HSCRRS	HSCRRS	2376 bp	mRNA	PRI	22-MAR-1995
LOCUS	Human CRL mRNA for C3b/C4b receptor	secreted form.			
DEFINITION	X1362.1 Y08012				
ACCESSION	X1362.1	GI:30197			
VERSION					
KEYWORDS	alternate splicing; C3b/C4b receptor; complement receptor;				

SOURCE	receptor.
ORGANISM	human.
JOURNAL TITLE	Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 2376)
AUTHORS	Hourcade,D.
JOURNAL	Direct Submission
TITLE	Submitted (29-Nov-1988) Hourcade D., Howard Hughes Medical Institute, 650 S. Euclid St. Louis Mo, 63110, USA
REFERENCES	2 (bases 1 to 2376) Hourcade,D., Mesner,D.R., Atkinson,J.P. and Holers,V.M. Identification of an alternative polyadenylation site in the human Cdb/Cdb receptor (complement receptor type 1) transcriptional unit and prediction of a secreted form of complement receptor type 1
MEDLINE	J. Exp. Med. 168 (4), 1255-1270 (1988) 89010527
COMMENT	The sequence overlaps with that reported by Klickestein et. al. in J. Exp. Med. 165:1095-1112(1987) x05309 and in J. Exp. Med. 168:1699-1717(1988).
FEATURES	location/Qualifiers
SOURCE	1..2376
CDS	/organism="Homo sapiens" /db_xref="taxon:9606" /haplo_type="CRI-A" /cell_line="HD-60" /clone="CRI-4" <1..1682 /note="CRI receptor precursor (AA -16 to 543) (1 ts 2nd base in codon)" /codon_start=3 /protein_id="CA32541.1" /db_xref="GI:736240" /translation="SILAVVLLALPYAMGQNAPEWLPAPRPNTLDEFPPIGTYL MYECREYSGRPSIITLKNSWTGAADRRKRSRPPPVNMGVHYIGIOFGSOI KISGTEKIRLLNGSSATCIISGDIVLNDSTPICDRIPLCPPTTNGDISTNRNF HYSVTVYRCNPGGSGKKVELVEGPSITYTSDDVDGVSGAPDCIIIPNKCTPNV ENGLISDNLSFLSLNEVFEFCOPGPVMKGPRVKCOALNKMEPELSCSRVCOAPP DVLAERTORDKDNFSPGEVFCEGYEDLRGAASMRCTPOGMSPRAATCEVKSCD DFMGOILLGVLPVNLIGAKYDVEDEFOLGSSASYCVLAGMSLNSSVPQE GIVCSPPRYVPCNGRHRTKPLEVYFPGAAVVYTDPRHRDRTSIDLGESITRCSDD QNGVSSPAPRGCLIGHCOAHPDLFKLLLTQTNASDFIGTLTKCYREPREYGRPS ITLCDNLWSSPPDYCKRKSKTPPDVNMGVHYTDIQVGSINVSCTTG"
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mat_peptide	
polya_site	/note="polya site" 2376
BASE COUNT	633 a 549 c 568 g 626 t
ORIGIN	
Query Match	75.7%; Score 447.2; DB 53; Length 2376;
Best Local Similarity	85.0%; Pred. No. 1,4e-129;
Matches 500; Conservative	0; Mismatches 88; Indels 0; Gaps 0;
Dy	4 CAGTCACAGCGTCCGGAATGGCTGCCGCGCGCCGCACCAACTGACTGATTAATT 63
Dy	111 111
Dy	51 CAATGCATATGCCCAAGATAGCTTCATTTCCAGAGGCTACCAACTGATGATGAGTT 110
Dy	64 GAGTCCCGCATCGGACTACTACTAACATAACAATGCCGCCGGGTTAATAGGGCGCCCG 123
Dy	111 111
Dy	111 GAGTTTCCCATTTGGACATATCTGAACATTAATAGCCGCCCTGGTTATTCGGGAAGACG 170
Dy	124 TTTTCTATCATCTGCCTCAAAAACCTCTCTCGAGACTGGTGTCTAAGAGACCCTTGCAGAGT 183
Dy	171 TTTTCTATCATCTGCCTCAAAAACCTCACTCTCGAGACTGGTGTCTAAGAGAGAGTGCAGAGCT 230
Dy	184 AATCTGTCTAATCCGCCAGATCCGGTTAAGCGCATGTGATGTGATCAAAGGCATC 243
Dy	231 AAATCATCTCTAATCCGCCAGATCCCTGTGAATGGCATGTGATGTGATCAAAGGCATC 290

MgCl ₂ :	2.5	mm
KCl:	50	mm
Tris-HCl:	20	mm
pH:	8.3	

Query Match	75.4%	Score 445.6	DB 51	Length 6044
Best Local Similarity	84.9%	Pred. No. 4,5e-129		
Matches 499	Conservative	0	Mismatches 89	Indels 0
				Gaps 0
0Y	4	CAGTCCAAAGCGTCCCGAAATGGCGCTGGCGTGGCGGCGCCACCAACTGACTGATGATTT	63	
Db	51	CAATGCATATGCCCCAGAAATGGCTTCCATTTCGACAGGCTTACCACTTAATCTGATGATTT	110	
0Y	64	GAGTTCGGATCGGTACCTTACCTGAACTAATGCAATGCGCGCGGGTTATAGCGGCCCGG	123	
Db	111	GAGTTTCCCATGGGACATATCTGAACATATGAAATGCGCGCGCTGTTATATATGGAAGACCG	170	
0Y	124	TTTTCTATCATCTGGCTGAAAACCTCTGTCTGAGCTAGGTGCTTAAGAGACCGTGGCAGCT	183	
Db	171	TTTTTATCATCTGGCTTAAAAACCTGAGCTGAGACGTGCTTAAGGACAGGTGACACGT	230	
0Y	184	AAATCTTGCGTAATCCCGCAGATCCGGTTAAGCGGATGTGATGATCAAGACATC	243	
Db	231	AAATCATTCGCTAATCCCTCAGATCTCTGGAATGGCATGTGCTGATCAAGACATC	290	
0Y	244	CAGTTGCGTTCGCCAATTAATATTTCTTACTAAAGGTTACCGTGTGATGGTTCTCC	303	
Db	291	CAATTCGATCCCAATTAATATTTCTTACTAAAGGATACGACTCATTTGGTTCTCG	350	
0Y	304	AGCGTACATGATCATCTCTGTGATTAATGTCATTTGGGATATATAACACCGATTTGT	363	
Db	351	TTCTGCACATGGATATCTCAGGTATGCTGATTTGGGATATATAACACCTATTTGT	410	
0Y	364	GACCAATTCCTGTGTGTGCTGCGCGCAGCATCCGCAAGGATGATTCACCTTACAGT	423	
Db	411	GACCAATTCCTGTGTGTGCTGCGCGCAGCATCCGCAAGGATGATTCACCTTACAGT	470	
0Y	424	CGCGATATTTTCACTATGTTCTGTGTGATGACCTTACCACTGCAATCTGGGTAGCCGTGT	483	
Db	471	AGAGAGAAATTTTCACTATGATGATCAGTGTGATGACCTTACCGTGCATCTCTGGAGCGGAGG	530	
0Y	484	AAAAAGGTGTGAGCTCTGCTGCTGAGCCGCTCCATCTACTGCACTAACAAGACATCAA	543	
Db	531	AGAAAGGTGTGTGAGCTCTGCTGCTGAGCCGCTCCATCTACTGCACTAACAAGACATCAA	590	
0Y	544	GTGGCATCTGGAGCGCGCCGCGCACCGCATGTGCATATCCCGAACAA	591	
Db	591	GTGGCATCTGGAGCGCGCCGCGCACCTCATGTGCATATCTTAACCAAA	638	
RESULT 13				
BABCORE	LOCUS	BABCORE	1688 bp	mrna
DEFINITION	Papio cynocephalus complement receptor mRNA, partial cds.	PRI	07-MAY-1996	
VERSION	L77977.1	GI:1301608		
KEYWORDS	complement C3b; complement receptor; glycoposphatidylinositol-linked protein.			
SOURCE	Papio cynocephalus cdna to mrna.			
ORGANISM	Papio cynocephalus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.			
AUTHORS	1 (bases 1 to 1688)			
TITLE	Birmingham, D.J., Logan, C.M., Shen, X.-P. and Chen, W.			
	The baboon erythrocyte complement receptor is a glycoposphatidyl inositol-linked protein encoded by a homologue of the human CRI-like genetic element			
	Unpublished (1996)			
JOURNAL	Location/Qualifiers			
FEATURES	1..1688			
	/organism="Papio cynocephalus"			
	/db_xref="taxon:9556"			
	/cell_type="erythrocyte"			
	/dev_stage="adult"			
	/tissue_type="bone marrow"			
	<1..>1688			
	<1..>1571			

			/note="homologue of human CRL-1 like genetic element"
			/codon_start=3
			/product="complement receptor"
			/protein_id="AA99004.1"
			/db_xref="GI:1301609"
			/translation="vVQRMGASSPRSPERYGPAPRLLRECCGSLAVYVLALPVA WGQCNAPEQLFARPTLITDMSDEFPVTLYKELPELVHGPSI IOLKNSWTSADK KCQRSCRNPKRDVPVNGVHV I KDIQFSQJNYSCNKRY I LSGNTVIND NEPIECIIIEICGLPFIANDFIESTREYEPGVSVTVRCILGSRKKLEFLVEPSI YCISKDOVGIMSGPAPOCIIPNKCMPNENGVYVNRCLGSRRKLEFLVEPSI MKGRHVOCALMWEHELPSRSRVCCPVPELLIGHEFTSPHDSRPOEVTVSCEPY DLRAASLHCTPGQDNHPAERICVAKCDDPELOLPNGRVLVPLNLDAKVSFCDE GFIRKAGFNASHCVIAGMKALMNSSVPAECEDIFCPNPAILNGRIALPDIPGKEV SYIDPPDRGMTVNLIIGESTIRCTSDPQGNVSSAPROEIVSPAGANDALIYGTLS SGTFLVFILFFLS"
BASE COUNT	413 a	427 c	411 g 437 t
ORIGIN			
Query Match	70.5%; Score 416.8; DB 51; Length 1688;		
Best Local Similarity	81.8%; Pred. No. 5e-120;		
Matches 481; Conservative	0; Mismatches 107; Indels 0; Gaps 0;		
Oy	4	CAGTGCAACGCTCCGGATGGCTGCCGTTGC GGCGCCGACCACCTGACTGATAATT	63
Db	141	CAMTGCAATGCCCGCGAACACCTTCATTTGCCAGCGCTACCAACCTAATGATCATCT	200
Oy	64	GAGTTCGCCGATCGGACCTACCTGAACAGCAATGCCCGGGGTTTANAGGGCGCCGCG	123
Db	201	GAGTTTTCCCCTGGGACATCTGTAAGTAGATGATGCCCTCCCTGTTATCATGAAAACCA	260
Oy	124	TTTTCTATCATCTGCCTGAAAAAACHCTGCTGAGATGGTGCTNAMGACCGTTGCCAGCT	183
Db	261	TTTTCTATCATCTGCCATAAAAAACGCACTGTGGAGAATGGCTGTAAGACAAGTGCACAGCT	320
Oy	184	AAATCTTGCTAATCCGCCACAGATCCGTTAAACGGCATGTGATGATCAAAGGATC	243
Db	321	AAATCATGTCTAATCCCTAAAGATCCTGTGAATGGCATGTGATGATCAAAGACATC	380
Oy	244	CAGTTCGGTCCCAATTAATTAATCTTGTTGCTAAAGTTTACCCTGATGGTCCGCC	303
Db	381	CAGTTCGGATCCCAATTAATTAATCTTGTTGATAAAGATTAACCGACTATTTGGTCTTCG	440
Oy	304	AGCGCTACATCATCATCTCTGTGTGATAGTCAATTTGGATTAATGAACAACCGATTGT	363
Db	441	TCCGCAATCATGATCATCTCAAGCAATCTGTCATTTGGATTAATGAACAACCTATTGT	500
Oy	364	GACCAATTCGCTGTGCTGTGCGCGCCGACATCCGCCAAGCGTATTCACCTCTATCACT	423
Db	501	GAGATTAATTCCTTGGGCGCTCACCCCCACATCCGCAATGGAGATTTCATTAGACACAGC	560
Oy	424	CGCGGATTTTTCATATGTTCTGTGTGTGATCACTCACTGCAATCTGGTAGCCGTGT	483
Db	561	AGAGGATATTTTCCCTACGAGATCCGTGTGATCTATTCCTGCAATCTTGGAGGCGGAAGG	620
Oy	484	AAAAAGGTGTTTGAAGCTGTGGGTAGAGCGTCACTCACTGACATGACGAAGAAGCATCAA	543
Db	621	AAAAAGCTGTTTGAAGCTGTGGGTAGAGCGTTCATATATCTGCACCAAGGAAGATACCAA	680
Oy	544	GTGGGATCTGTGGAGCGCGCCGACCGACGATGATCATCCGGAAACAA	591
Db	681	GTGGGATCTGTGGAGCGCGCCGACCGACGATGATTAACCAACAA	728
RESULT 14			
BABCOREA			
LOCUS	BABCOREA	945 bp	mRNA
DEFINITION	Papio cynocephalus complement receptor mRNA, partial cds.		
ACCESSION	L77978		
VERSION	L77978.1	GI:1301610	
KEYWORDS	complement C3b; complement receptor; glycophosphatidylinositol-linked protein. Papio cynocephalus cdna to mRNA.		
SOURCE			

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PT Soluble polypeptide comprising short consensus repeats from LHR-A -
PT used to treat disorders and diseases associated with inflammation or
XX inappropriate complement activation
PS Claim 13; Page 42; 67pp; English.
XX
CC This is the amino acid sequence of CM7, a protein that consists
CC of the short consensus repeats (SCR) 1 and 2 from the complement
CC receptor type 1 (CRI) fused to the SCR3 of CRI-like protein (see
CC W9247). CM7 DNA (see V53262) was constructed using pDB1013-5,
CC which codes for SCR1-3 of CRI, by site-directed mutagenesis that
CC resulted in the introduction of 10 amino acid changes to the native
CC SCR3 sequence corresponding to changes observed in the protein
CC encoded by the CRI-like pseudogene (crispse). The DNA construct
CC in plasmid pProcCRI-3CM7 was used to transform *Escherichia coli*
CC BL21(DE3) cells, and CM7 was purified from solubilised inclusion
CC bodies. The invention provides DNA sequences (see V53262 and
CC V53269-79) encoding novel soluble engineered CRI polypeptides (see
CC W53236-47) such as CM7 that act as complement inhibitors with
CC functional complement inhibitory, including anti-haemolytic,
CC activity. These can be used to treat a disease or disorder
CC associated with inflammation or inappropriate complement activation,
CC such as neurological disorders (e.g. multiple sclerosis and
CC Parkinson's disease), disorders of inappropriate or undesirable
CC complement activation (e.g. xenograft rejection), inflammatory
CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),
CC post-ischaemic reperfusion conditions, infection or sepsis,
CC immune complex disorders and autoimmune diseases (e.g. rheumatoid
CC arthritis, proliferative nephritis and myasthenia gravis), and
CC reproductive disorders.
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1104; DB 19; Length 197;
Best Local Similarity 100.0%; Pred. No. 2,4e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQCNAPFWLPAPRPTNLDFEFPPIGTLYLNECRPGYSGRPFSLICLNQSVWTGAKDKCR 60
DB 1 mqcnapewlpfarpntldfepfigtlylneecrpgysgrpsfslclnqsvwtgkdkrcr 60

QY 61 RKSCRNPDPVNGVHWIKIGIOFSQIKYSCCTKGRILIGSSATCISGDTVIMDNETPI 120
DB 61 rkscrnppdpvngvhwikigiofsqikyscctkgyrilgssatclisgdtvimeetpi 120

QY 121 CDRIPCGLPPTIANGDFTSISREYFHGVSVTYHNCNLGSRGKRYFELVGEPSITCTSKDD 180
DB 121 cdripcglpptiangdftsisisreyfhgvsvttyhcnlgsrgkryfelvgepsitctskdd 180

QY 181 QVGIMSGPAPQCIIIPNK 197
DB 181 qvgiwsgapqciiipnk 197

RESULT 2
W75986 ID W75986 standard; Protein; 198 AA.
XX
AC W75986;
XX
DT 18-JAN-1999 (first entry)
XX
DE Complement receptor type 1-like polypeptide CM7/Cys.
XX
KM Complement receptor type-1; CRI; CM7/Cys; complement; inhibitor;
KM anti-haemolytic; multiple sclerosis; Parkinson's disease;
KM xenograft rejection; inflammation; Crohn's disease; asthma;
KM pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KM autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KM myasthenia gravis; reproductive disorder; therapy.
XX
OS Homo sapiens.

OS Synthetic.
XX
PN WO9839433-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-GB00727.
XX
PR 05-MAR-1997; 97GB-0004519.
XX
PA (ADPR-) ADPROTECH PLC.
XX
PI Cox VE, Mossakowska DEI, Smith RAG;
XX WPI; 1998-506358/43.
DR
XX
PT Soluble polypeptide comprising short consensus repeats from LHR-A -
PT used to treat disorders and diseases associated with inflammation or
PT inappropriate complement activation
PS Claim 19; Page 51-52; 67pp; English.
XX
XX This is the amino acid sequence of CM7/Cys, a protein that consists
XX of the short consensus repeats (SCR) 1 and 2 from the complement
XX receptor type 1 (CRI) fused to the SCR3 of CRI-like protein (see
XX W9247) and having an additional C-terminal Cys residue. CM7/Cys
XX DNA was constructed by site-directed mutagenesis (see V53280)
XX of pProcCRI-3CM7 (see V53262). This plasmid was used to transform
XX *Escherichia coli*, and CM7/Cys was purified from solubilised
XX inclusion bodies. The invention provides novel soluble engineered
XX polypeptides (see W53236-47 and W75986-94) such as CM7/Cys that act
XX as complement inhibitors with functional complement inhibitory,
XX including anti-haemolytic, activity. These can be used to treat a
XX disease or disorder associated with inflammation or inappropriate
XX complement activation, such as neurological disorders (e.g.
XX multiple sclerosis, Parkinson's disease), disorders of inappropriate
XX complement activation (e.g. Crohn's disease, asthma, and acute
XX inflammatory disorders (e.g. Crohn's disease, asthma, and acute
XX pancreatitis), post-ischaemic reperfusion conditions, infection or
XX sepsis, immune complex disorders and autoimmune diseases (e.g.
XX rheumatoid arthritis, proliferative nephritis and myasthenia
XX gravis), and reproductive disorders.
XX
SQ Sequence 198 AA;

Query Match 100.0%; Score 1104; DB 19; Length 198;
Best Local Similarity 100.0%; Pred. No. 2,4e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQCNAPFWLPAPRPTNLDFEFPPIGTLYLNECRPGYSGRPFSLICLNQSVWTGAKDKCR 60
DB 1 mqcnapewlpfarpntldfepfigtlylneecrpgysgrpsfslclnqsvwtgkdkrcr 60

QY 61 RKSCRNPDPVNGVHWIKIGIOFSQIKYSCCTKGRILIGSSATCISGDTVIMDNETPI 120
DB 61 rkscrnppdpvngvhwikigiofsqikyscctkgyrilgssatclisgdtvimeetpi 120

QY 121 CDRIPCGLPPTIANGDFTSISREYFHGVSVTYHNCNLGSRGKRYFELVGEPSITCTSKDD 180
DB 121 cdripcglpptiangdftsisisreyfhgvsvttyhcnlgsrgkryfelvgepsitctskdd 180

QY 181 QVGIMSGPAPQCIIIPNK 197
DB 181 qvgiwsgapqciiipnk 197

RESULT 3
W75993 ID W75993 standard; Protein; 211 AA.
XX
AC W75993;
XX

DT 18-JAN-1999 (first entry)
 XX
 DE Complement receptor type 1-like polypeptide CW7rgdcys.
 XX
 KW Complement receptor type-1; CRI; CM7; complement; inhibitor;
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;
 KW xenograft rejection; inflammation; Crohn's disease; asthma;
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;
 KW myasthenia gravis; reproductive disorder; therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN MO9839433-A1.
 XX
 PD 11-SEP-1998.
 XX
 PD 05-MAR-1998; 98WO-GB00727.
 XX
 PF 05-MAR-1997; 97GB-0004519.
 XX
 PR (ADPR-) ADPROTECH PLC.
 XX
 PA Cox VF, Mossakowska DEI, Smith RAG;
 PI WPI; 1998-506358/43.
 DR
 XX
 PT Soluble polypeptide comprising short consensus repeats from LHR-A -
 PT used to treat disorders and diseases associated with inflammation or
 PT inappropriate complement activation
 XX
 PS Claim 19; Page 57; 67pp; English.
 XX
 CC This is the amino acid sequence of CW7rgdcys, a protein that
 CC consists of the short consensus repeats (SCR) 1 and 2 from the
 CC complement receptor type 1 (CRI) fused to the SCR3 of CRI-like
 CC protein (see W9236), and additionally having a C-terminal RGD
 CC sequence as a ligand for the glycoprotein IIb/IIIa of platelets.
 CC CW7rgdcys was expressed in Escherichia coli from plasmid
 CC pBrosScri-3CM7rgdcys. The invention provides novel soluble
 CC CRI derivatives (see W9236-47 and W5986-94) that act as
 CC complement inhibitors with functional complement inhibitory,
 CC including anti-haemolytic, activity. These can be used to treat a
 CC disease or disorder associated with inflammation or inappropriate
 CC complement activation, such as neurological disorders (e.g.
 CC multiple sclerosis and Parkinson's disease), disorders of
 CC inappropriate or undesirable complement activation (e.g. xenograft
 CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,
 CC infection or sepsis, immune complex disorders and autoimmune
 CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and
 CC myasthenia gravis), and reproductive disorders.
 CC
 XX
 SO Sequence 211 AA;

Query Match 100.0%; Score 1104; DB 19; Length 211;
 Best Local Similarity 100.0%; Pred. No. 2.6e-99;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOCNAPEMLFAPRTNLTDFEPPIGTYLWTECPGSGRPFSTICLKNSVWTGANDRCR 60
 DB 1 mqcnawepjfarptnltdfeipdtylwyecpysgrpfsticlknswtgakdrcr 60
 QY 61 RKSCRNPPDVGNGMVAHYIKIOFGSOIKYCTKGRILIGSSASACIIISGDPVINDNTP 120
 DB 61 rkscrrppdpvgngmvahtkifgsgqkysctkyrlligssasacilsgdtvawdncpi 120
 QY 121 CDRIPGCLPPTIANGDFTSISREYFHGSVVYTHCNLGSRRKVFELVGPESIVCTSKDP 180
 DB 121 cdrilpcglppltiangdftsistreyfhygsvvlythcnlgsrgkxvfelvgpslyciskdd 180

QY 181 QVGIWSPAPQCITIPNK 197
 DB 181 qvgiwsqapqcitipnk 197

RESULT 4
 ID W75994 standard; Protein; 214 AA.
 XX
 AC W75994;
 XX
 DT 18-JAN-1999 (first entry)
 XX
 DE Complement receptor type 1-like polypeptide CW7Tcell.
 XX
 KW Complement receptor type-1; CRI; CM7/Tcell; complement; inhibitor;
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;
 KW xenograft rejection; inflammation; Crohn's disease; asthma;
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;
 KW myasthenia gravis; reproductive disorder; therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN MO9839433-A1.
 XX
 PD 11-SEP-1998.
 XX
 PD 05-MAR-1998; 98WO-GB00727.
 XX
 PF 05-MAR-1997; 97GB-0004519.
 XX
 PR (ADPR-) ADPROTECH PLC.
 XX
 PA Cox VF, Mossakowska DEI, Smith RAG;
 PI WPI; 1998-506358/43.
 DR
 XX
 PT Soluble polypeptide comprising short consensus repeats from LHR-A -
 PT used to treat disorders and diseases associated with inflammation or
 PT inappropriate complement activation
 XX
 PS Claim 19; Page 58; 67pp; English.
 XX
 CC This is the amino acid sequence of CW7Tcell, a protein that
 CC consists of the short consensus repeats (SCR) 1 and 2 from the
 CC complement receptor type 1 (CRI) fused to the SCR3 of CRI-like
 CC protein (see W9236), and additionally having a C-terminal
 CC extension that targets the protein to the T-cell receptor alpha
 CC subunit. CW7Tcell was expressed in Escherichia coli from plasmid
 CC pBrosScri-3CM7Tcell. The invention provides novel soluble
 CC CRI derivatives (see W9236-47 and W5986-94) that act as
 CC complement inhibitors with functional complement inhibitory,
 CC including anti-haemolytic, activity. These can be used to treat a
 CC disease or disorder associated with inflammation or inappropriate
 CC complement activation, such as neurological disorders (e.g.
 CC multiple sclerosis and Parkinson's disease), disorders of
 CC inappropriate or undesirable complement activation (e.g. xenograft
 CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,
 CC and acute pancreatitis), post-ischaemic reperfusion conditions,
 CC infection or sepsis, immune complex disorders and autoimmune
 CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and
 CC myasthenia gravis), and reproductive disorders.
 CC
 XX
 SO Sequence 214 AA;

Query Match 100.0%; Score 1104; DB 19; Length 214;
 Best Local Similarity 100.0%; Pred. No. 2.7e-99;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOCNAPEMLFAPRTNLTDFEPPIGTYLWTECPGSGRPFSTICLKNSVWTGANDRCR 60

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Db      1  mgnapewlpfarpnltdfeifpigtynecrpsygrpfslclksnwtgkdr 60
QY      61  RKSCHNPPDPVNGMVAHVIGIQFGSOIKRSCYKGYRLIGSSATCIISGDTVIMDNEPPI 120
Db      61  rkschnppdpvngmva hvikgigfsgskysctkgyrligssatciisgdtv imdneptl 120
QY      121 CDRIPCGLPPTIANGDFTSIREYFHGSAVWYHCLSGRKKVFEVLGEPSTICTSKDD 180
Db      121 cdripcglpptiangdftsireyfhgsavvlyhcnlsgrgkvfelvgepslyctskdd 180
QY      181 QVGIMSGAPQCIIPNK 197
Db      181 gvgiwsqpapqcilpnk 197

RESULT  5
W75987  ID W75987 standard; Protein; 215 AA.
AC      W75987;
DE      18-JAN-1999 (first entry)
XX      Complement receptor type 1-like polypeptide PM-9.
KM      Complement receptor type-1; CRI; CM7; PM-9; complement; inhibitor;
KM      myristoyl/electrostatic switch peptide reagent 1; MSMP-1;
KM      anti-haemolytic; multiple sclerosis; Parkinson's disease;
KM      xenograft rejection; inflammation; Crohn's disease; asthma;
KM      pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KM      autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KM      myasthenia gravis; reproductive disorder; therapy.
OS      Chimeric - Homo sapiens.
XX      Chimeric - Synthetic.
FH      Key
FT      Protein
FT      Location/Qualifiers
FT      1..197
FT      /label= CM7
FT      Peptide
FT      199..215
FT      /label= MSMP-1
FT      Disulfide-bond
FT      198..199
FT      Modified-site
FT      199
FT      /note= "(S-2-thiopyridyl)cysteine"
FT      Modified-site
FT      215
FT      /note= "N-(myristoyl)-glycine"
XX      W09839433-A1.
XX      PD 11-SEP-1998.
XX      PF 05-MAR-1998; 98WO-GB00727.
XX      PR 05-MAR-1997; 97GB-0004519.
XX      PA (ADPR-) ADPROTECH PLC.
XX      PI Cox VF, Mossakowska DEI, Smith RAG;
XX      WPI; 1998-506358/43.
XX      DR
XX      PT Soluble polypeptide comprising short consensus repeats from LHR-A -
XX      PT used to treat disorders and diseases associated with inflammation or
XX      PT inappropriate complement activation
XX      PS
XX      Claim 17: Page 52-53; 67pp; English.
XX      This is the amino acid sequence of PM-1, or (CM7)-Cys-S-S-(MSMP-1),
XX      comprising novel soluble complement receptor type 1 (CRI)-like
XX      polypeptide CM7 (see W79236) joined to a myristoyl/electrostatic
XX      switch peptide reagent 1 (MSMP-1). It was produced by coupling
XX      CM7/Cys (see W75985) to a synthetic MSMP-1 peptide. CM7 comprises

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CC      the short consensus repeats (SCR) 1 and 2 from CRI and SCR3 of the
CC      CRI-like protein (see W79247). Soluble CRI-derived proteins of the
CC      invention (see W53236-47 and W75987-94) act as complement inhibitors
CC      with functional complement inhibitory, including anti-hemolytic,
CC      activity. These can be used to treat a disease or disorder
CC      associated with inflammation or inappropriate complement activation,
CC      such as neurological disorders (e.g. multiple sclerosis, Parkinson's
CC      disease), disorders of inappropriate or undesirable complement
CC      activation (e.g. xenograft rejection), inflammatory disorders (e.g.
CC      Crohn's disease, asthma, and acute pancreatitis), post-ischaemic
CC      reperfusion conditions, infection or sepsis, immune complex
CC      disorders and autoimmune diseases (e.g. rheumatoid arthritis,
CC      proliferative nephritis and myasthenia gravis), and reproductive
CC      disorders.
XX      SQ Sequence 215 AA;

Query Match      100.0%; Score 1104; DB 19; Length 215;
Best Local Similarity 100.0%; Pred. No. 2,7e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MQCNAPEWLPFARPNTLDEFEFPFGTYLNEYCRGSGRPFSTICLKNVWTGAKR 60
Db      1  mgnapewlpfarpnltdfeifpigtynecrpsygrpfslclksnwtgkdr 60
QY      61  RKSCHNPPDPVNGMVAHVIGIQFGSOIKRSCYKGYRLIGSSATCIISGDTVIMDNEPPI 120
Db      61  rkschnppdpvngmva hvikgigfsgskysctkgyrligssatciisgdtv imdneptl 120
QY      121 CDRIPCGLPPTIANGDFTSIREYFHGSAVWYHCLSGRKKVFEVLGEPSTICTSKDD 180
Db      121 cdripcglpptiangdftsireyfhgsavvlyhcnlsgrgkvfelvgepslyctskdd 180
QY      181 QVGIMSGAPQCIIPNK 197
Db      181 gvgiwsqpapqcilpnk 197

RESULT  6
W79240  ID W79240 standard; Protein; 197 AA.
AC      W79240;
DE      18-JAN-1999 (first entry)
XX      Complement receptor type 1-like protein CM5.
KM      Complement receptor type-1; CRI; CM5; complement; inhibitor;
KM      anti-haemolytic; multiple sclerosis; Parkinson's disease;
KM      xenograft rejection; inflammation; Crohn's disease; asthma;
KM      pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KM      autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KM      myasthenia gravis; reproductive disorder; therapy.
OS      Homo sapiens.
XX      Synthetic.
FH      Key
FT      Protein
FT      Location/Qualifiers
FT      1..197
FT      /label= CM5
FT      Peptide
FT      199..215
FT      /label= MSMP-1
FT      Disulfide-bond
FT      198..199
FT      Modified-site
FT      199
FT      /note= "(S-2-thiopyridyl)cysteine"
FT      Modified-site
FT      215
FT      /note= "N-(myristoyl)-glycine"
XX      W09839433-A1.
XX      PD 11-SEP-1998.
XX      PF 05-MAR-1998; 98WO-GB00727.
XX      PR 05-MAR-1997; 97GB-0004519.
XX      PA (ADPR-) ADPROTECH PLC.
XX      PI Cox VF, Mossakowska DEI, Smith RAG;
XX      WPI; 1998-506358/43.
XX      DR N-PSDB; V53272.

```

XX Soluble polypeptide comprising short consensus repeats from LHR-A -
PT used to treat disorders and diseases associated with inflammation or
PT inappropriate complement activation
XX
XX Claim 13; Page 46-47; 67pp; English.
XX
CC This is the amino acid sequence of CM5, a protein that consists
CC of the short consensus repeats (SCR) 1 and 2 from complement
CC receptor type 1 (CRI) fused to an SCR3 (see W79245) in which 5 amino
CC acids were altered to those found in the SCR3 of the encoded protein
CC of the CRI-like pseudogene (Cripse). CM5 DNA (see V53272) was
CC constructed by site-directed mutagenesis (see V53264-65) of plasmid
CC pDB1013-5, which codes for SCR1-3 of CRI. pProSCR1-3CM5 carrying
CC CM5 DNA was used to transform *Escherichia coli* BL21(DE3), and CM5
CC was purified from solubilised inclusion bodies. The invention
CC provides DNA sequences (see V53262 and V53269-79) encoding novel
CC soluble engineered CRI polypeptides (see W53236-47) such as CM5
CC that act as complement inhibitors with functional complement
CC inhibitory, including anti-haemolytic, activity. These can be used
CC to treat a disease or disorder associated with inflammation or
CC inappropriate complement activation, such as neurological disorders
CC (e.g. multiple sclerosis and Parkinson's disease), disorders of
CC inappropriate or undesirable complement activation (e.g. xenograft
CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,
CC and acute pancreatitis), post-ischaemic reperfusion conditions,
CC infection or sepsis, immune complex disorders and autoimmune
CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and
CC myasthenia gravis), and reproductive disorders.
XX
SQ Sequence 197 AA:

Query Match 97.7%; Score 1079; DB 19; Length 197;
Best Local Similarity 98.0%; Pred. No. 6.3e-97;
Matches 193; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MOCNAPFELPFPARTNTDFFEPFGTYLNEYECRPGSGRPFSTICAKNSWTGAKRCR 60
DB 1 mqcnapewlpfarpntndfelfpdylylneecrpgsgpfsticaknswtgakrcr 60
QY 61 RKSQRNPDPVNGMVHVIKIQFGSQIKYCTGKGYRLIGSSSATCIIISGDTVMINDNTP 120
DB 61 rkscrnppdpvngmvhvikiqfgsqikyctgkgyrligsssatcIIISGDTVMINDNTP 120
QY 121 CDRIPCGLPPTIANGDFTSISREYFHYSVYTHCNLGSRGKVFELVGPESIVCTSKD 180
DB 121 cdripcglppltiangdftsIsreyfhyssvtythcnlgsgkvvfelvgpesivctskd 180
QY 181 QVGWISGPAPOCIIIPNK 197
DB 181 qvgwIsGpApocIIPnk 197

RESULT 7
W79241
ID W79241 standard; Protein; 197 AA.
XX
AC W79241:
XX
DT 18-JAN-1999 (first entry)
XX
XX Complement receptor type 1-like protein CM6.
XX
XX Complement receptor type-1; CRI; CM6; complement's inhibitor;
XX anti-haemolytic; multiple sclerosis; Parkinson's disease;
XX xenograft rejection; inflammation; Crohn's disease; asthma;
XX pancreatitis; post-ischaemic reperfusion; infection; sepsis;
XX autoimmune disease; rheumatoid arthritis; proliferative nephritis;
XX myasthenia gravis; reproductive disorder; therapy.
XX
OS Homo sapiens.
OS
OS Synthetic.

XX
XX MO9839433-A1.
XX
XX 11-SEP-1998.
XX
XX 05-MAR-1998; 98WO-GB00727.
XX
XX 05-MAR-1997; 97GB-0004519.
XX
XX (ADPR-) ADPROTECH PLC.
XX
XX Cox VE, Mossakowska DEI, Smith RAG;
XX WPI, 1998-506358/43.
XX N-PSDB; V53273.
XX
XX Soluble polypeptide comprising short consensus repeats from LHR-A -
XX used to treat disorders and diseases associated with inflammation or
XX inappropriate complement activation
XX
XX Claim 13; Page 47-48; 67pp; English.
XX
CC This is the amino acid sequence of CM6, a protein that consists
CC of the short consensus repeats (SCR) 1 and 2 from complement
CC receptor type 1 (CRI) fused to an SCR3 (see W79246) in which 6 amino
CC acids were altered to those found in the SCR3 of the encoded protein
CC of the CRI-like pseudogene (Cripse). CM6 DNA (see V53273) was
CC constructed by site-directed mutagenesis (see V53263 and V53265) of
CC pDB1013-5, which codes for SCR1-3 of CRI. pProSCR1-3CM6 carrying
CC CM6 DNA was used to transform *Escherichia coli* BL21(DE3), and CM6
CC was purified from solubilised inclusion bodies. The invention
CC provides DNA sequences (see V53262 and V53269-79) encoding novel
CC soluble engineered CRI polypeptides (see W53236-47) such as CM6
CC that act as complement inhibitors with functional complement
CC inhibitory, including anti-haemolytic, activity. These can be used
CC to treat a disease or disorder associated with inflammation or
CC inappropriate complement activation, such as neurological disorders
CC (e.g. multiple sclerosis and Parkinson's disease), disorders of
CC inappropriate or undesirable complement activation (e.g. xenograft
CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,
CC and acute pancreatitis), post-ischaemic reperfusion conditions,
CC infection or sepsis, immune complex disorders and autoimmune
CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and
CC myasthenia gravis), and reproductive disorders.
XX
SQ Sequence 197 AA:

Query Match 97.6%; Score 1077; DB 19; Length 197;
Best Local Similarity 97.5%; Pred. No. 9.9e-97;
Matches 192; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MOCNAPFELPFPARTNTDFFEPFGTYLNEYECRPGSGRPFSTICAKNSWTGAKRCR 60
DB 1 mqcnapewlpfarpntndfelfpdylylneecrpgsgpfsticaknswtgakrcr 60
QY 61 RKSQRNPDPVNGMVHVIKIQFGSQIKYCTGKGYRLIGSSSATCIIISGDTVMINDNTP 120
DB 61 rkscrnppdpvngmvhvikiqfgsqikyctgkgyrligsssatcIIISGDTVMINDNTP 120
QY 121 CDRIPCGLPPTIANGDFTSISREYFHYSVYTHCNLGSRGKVFELVGPESIVCTSKD 180
DB 121 cdripcglppltiangdftsIsrenfhyssvtythcnlgsgkvvfelvgpesivctskd 180
QY 181 QVGWISGPAPOCIIIPNK 197
DB 181 qvgwIsGpApocIIPnk 197

RESULT 8
W79237
ID W79237 standard; Protein; 197 AA.
XX

AC W79237;
XX
DT 18-JAN-1999 (first entry)
XX
DE Complement receptor type 1-like protein CMI.
XX
KW Complement receptor type-1; CMI; complement; inhibitor;
KW anti-haemolytic; multiple sclerosis; Parkinson's disease;
KW xenograft rejection; inflammation; Crohn's disease; asthma;
KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KW myasthenia gravis; reproductive disorder; therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN MO9839433-A1.
XX
PD 11-SEP-1998.
XX
PE 05-MAR-1998; 98WO-GB00727.
XX
PR 05-MAR-1997; 97GB-0004519.
XX
PA (ADPR-) ADPROTECH PLC.
XX
PI Cox VF, Mossakowska DEI, Smith RAG;
XX
DR WPI: 1998-506358/43.
DR N-PSDB: V53269.
XX
PT Soluble polypeptide comprising short consensus repeats from LHR-A -
PT used to treat disorders and diseases associated with inflammation or
PT inappropriate complement activation
XX
PS Claim 13; Page 44; 67pp: English.
XX
CC This is the amino acid sequence of CMI, a protein that consists
CC of the short consensus repeats (SCR) 1 and 2 from complement
CC receptor type 1 (CRI) fused to an SCR3 (see W79242) in which 5 amino
CC acids were altered to those found in the SCR3 of the encoded protein
CC of the CRI-like pseudogene (Cripse). CMI DNA (see V53269) was
CC constructed by site-directed mutagenesis (see V53263) of plasmid
CC pBI013-5, which codes for SCR1-3 of CRI. pBROCCRI-3CMI carrying
CC CMI DNA was used to transform Escherichia coli BL21(DE3), and CMI
CC was purified from solubilised inclusion bodies. The invention
CC provides DNA sequences (see V53262 and V53269-79) encoding novel
CC soluble engineered CRI polypeptides (see W53236-47) such as CMI
CC that act as complement inhibitors with functional complement
CC inhibitory, including anti-haemolytic, activity. These can be used
CC to treat a disease or disorder associated with inflammation or
CC inappropriate complement activation, such as neurological disorders
CC (e.g. multiple sclerosis and Parkinson's disease), disorders of
CC inappropriate or undesirable complement activation (e.g. xenograft
CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,
CC and acute pancreatitis), post-ischaemic reperfusion conditions,
CC infection or sepsis, immune complex disorders and autoimmune
CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and
CC myasthenia gravis), and reproductive disorders.
XX
SQ Sequence 197 AA;
Query Match 97.3%; Score 1074; DB 19; Length 197;
Best Local Similarity 97.5%; Pred. No. 1.9e-96;
Matches 192; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MOCNAPENLPPARPNTLDEFEFFIGTYINTECRPGYSGRPFSITLKNVYTGAKDCR 60
Db 1 mqcnapewlparpnltdefefpigtynntecrpqysgrfslclnsvwtgskdcr 60
QY 61 RKSGRNPDPVNGWYHVKGIOFGSOIYSCTKGRRLIGSSAGNCITGDIYVMDNETPI 120
|||||

Db 61 rksgrnpdpvngwyhvkgiofgsqikysctkgryllgssatclsgdtvwdnetpi 120
QY 121 CDRIPCGLPPIIANGDFISREFFHSGVVTYHCNLSGRKKYPELVGEPSITCTSND 180
|||||
Db 121 cdripccgippliangdfisireyfhysvvtlycnpbgsgkrkfelvgepslyctsnd 180
QY 181 QVGISGAPQCIIIPNK 197
Db 181 qvgiwsgapqcilpnk 197
RESULT 9
W79238
ID W79238 standard; Protein; 197 AA.
XX
AC W79238;
XX
DT 18-JAN-1999 (first entry)
XX
DE Complement receptor type 1-like protein CM2.
XX
KW Complement receptor type-1; CRI; CM2; complement; inhibitor;
KW anti-haemolytic; multiple sclerosis; Parkinson's disease;
KW xenograft rejection; inflammation; Crohn's disease; asthma;
KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KW myasthenia gravis; reproductive disorder; therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN MO9839433-A1.
XX
PD 11-SEP-1998.
XX
PE 05-MAR-1998; 98WO-GB00727.
XX
PR 05-MAR-1997; 97GB-0004519.
XX
PA (ADPR-) ADPROTECH PLC.
XX
PI Cox VF, Mossakowska DEI, Smith RAG;
XX
DR WPI: 1998-506358/43.
DR N-PSDB: V53270.
XX
PT Soluble polypeptide comprising short consensus repeats from LHR-A -
PT used to treat disorders and diseases associated with inflammation or
PT inappropriate complement activation
XX
PS Claim 13; Page 44-45; 67pp: English.
XX
CC This is the amino acid sequence of CM2, a protein that consists
CC of the short consensus repeats (SCR) 1 and 2 from complement
CC receptor type 1 (CRI) fused to an SCR3 (see W79243) in which 4 amino
CC acids were altered to those found in the SCR3 of the encoded protein
CC of the CRI-like pseudogene (Cripse). CM2 DNA (see V53270) was
CC constructed by site-directed mutagenesis (see V53264) of plasmid
CC pBI013-5, which codes for SCR1-3 of CRI. pBROCCRI-3CM2 carrying
CC CM2 DNA was used to transform Escherichia coli BL21(DE3), and CM2
CC was purified from solubilised inclusion bodies. The invention
CC provides DNA sequences (see V53262 and V53269-79) encoding novel
CC soluble engineered CRI polypeptides (see W53236-47) such as CM2
CC that act as complement inhibitors with functional complement
CC inhibitory, including anti-haemolytic, activity. These can be used
CC to treat a disease or disorder associated with inflammation or
CC inappropriate complement activation, such as neurological disorders
CC (e.g. multiple sclerosis and Parkinson's disease), disorders of
CC inappropriate or undesirable complement activation (e.g. xenograft
CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,
CC and acute pancreatitis), post-ischaemic reperfusion conditions,
CC infection or sepsis, immune complex disorders and autoimmune
CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and

CC myasthenia gravis), and reproductive disorders.
 XX
 SO Sequence 197 AA:

Query Match 97.1%; Score 1072; DB 19; Length 197;
 Best Local Similarity 97.0%; Pred. No. 3e-96;
 Matches 191; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MOCNAPEMLPFARPTNLNDEFEFPIGTIYNTCEKRGYSGRPSIICLKNSWTGAKDRCR 60
 Db 1 mcnapewlfparpnltdfeipigtlylneecrpygrpfslclknsvtgakdrccr 60
 QY 61 RKSCHNPDPVNGMWHVIRIGIOFGSOIKKSCYKGRLLISSATCISDITYMNEPTPI 120
 Db 61 rkscnnpdpvngmwhvirigifgsgikysckgyrllyssatclisgdtvlywnepcpi 120
 QY 121 CDRIPCGLPPTIANGDFTSISREYFHYSVVTYHGNLGRGKRVFELVGEPSIYCTSKDD 180
 Db 121 cdripcgllpplltngdfistrenfnhysvvtlyrcmpsggrkrfvelvgepslyctskdnd 180
 QY 181 OVGIMSGRAPQCIIIPNK 197
 Db 181 gvgiwsppapgcilipnk 197

RESULT 10
 ID W79239 standard; Protein: 197 AA.
 AC W79239;

DT 18-JAN-1999 (first entry)
 DE Complement receptor type 1-like protein CM3.

XX Complement receptor type-1; CRI; CM3; complement; inhibitor;
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;
 KW xenograft rejection; inflammation; Crohn's disease; asthma;
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;
 KW myasthenia gravis; reproductive disorder; therapy.

XX Homo sapiens.
 OS Synthetic.

XX WO9839433-A1.

PD 11-SEP-1998.

PF 05-MAR-1998; 98WO-GB00727.

PR 05-MAR-1997; 97GB-0004519.

PA (ADPR-) ADPROTECH PLC.

PI Cox VF, Mossakowska DEL, Smith RAG;

XX WPI: 1998-506358/43.

DR N-PSDB: V53271.

PT Soluble polypeptide comprising short consensus repeats from LHR-A -
 PI used to treat disorders and diseases associated with inflammation or
 PI inappropriate complement activation

XX Claim 13; Page 45-46; 67pp; English.

XX This is the amino acid sequence of CM3, a protein that consists
 CC of the short consensus repeats (SCR) 1 and 2 from complement
 CC receptor type 1 (CRI) fused to an SCR3 (see W79244) in which 1 amino
 CC acid was altered to that found in the SCR3 of the encoded protein
 CC of the CRI-like pseudogene (Cripse). CM3 DNA (see V53271) was
 CC constructed by site-directed mutagenesis (see V53265) of plasmid

CC PDB1013-5, which codes for SCR1-3 of CRI. pBiosCR1-CM3 carrying
 CC CM3 DNA was used to transform Escherichia coli BL21(DE3), and CM3
 CC was purified from solubilised inclusion bodies. The invention
 CC provides DNA sequences (see V53262 and V53269-79) encoding novel
 CC soluble engineered CRI polypeptides (see W53236-47) such as CM3
 CC that act as complement inhibitors with functional complement
 CC inhibitory, including anti-haemolytic, activity. These can be used
 CC to treat a disease or disorder associated with inflammation or
 CC inappropriate complement activation, such as neurological disorders
 CC (e.g. multiple sclerosis and Parkinson's disease), disorders of
 CC inappropriate or undesirable complement activation (e.g. xenograft
 CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,
 CC and acute pancreatitis), post-ischaemic reperfusion conditions,
 CC infection or sepsis, immune complex disorders and autoimmune
 CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and
 CC myasthenia gravis), and reproductive disorders.

SO Sequence 197 AA:

Query Match 95.3%; Score 1052; DB 19; Length 197;
 Best Local Similarity 95.4%; Pred. No. 2.6e-94;
 Matches 188; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MOCNAPEMLPFARPTNLNDEFEFPIGTIYNTCEKRGYSGRPSIICLKNSWTGAKDRCR 60
 Db 1 mcnapewlfparpnltdfeipigtlylneecrpygrpfslclknsvtgakdrccr 60
 QY 61 RKSCHNPDPVNGMWHVIRIGIOFGSOIKKSCYKGRLLISSATCISDITYMNEPTPI 120
 Db 61 rkscnnpdpvngmwhvirigifgsgikysckgyrllyssatclisgdtvlywnepcpi 120
 QY 121 CDRIPCGLPPTIANGDFTSISREYFHYSVVTYHGNLGRGKRVFELVGEPSIYCTSKDD 180
 Db 121 cdripcgllpplltngdfistrenfnhysvvtlyrcmpsggrkrfvelvgepslyctskdnd 180
 QY 181 OVGIMSGRAPQCIIIPNK 197
 Db 181 gvgiwsppapgcilipnk 197

RESULT 11
 ID W75991 standard; Protein: 198 AA.
 AC W75991;

DT 18-JAN-1999 (first entry)

DE Complement receptor type 1-like polypeptide CM16/cys.

XX Complement receptor type-1; CRI; CM16; complement; inhibitor;
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;
 KW xenograft rejection; inflammation; Crohn's disease; asthma;
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;
 KW myasthenia gravis; reproductive disorder; therapy.

XX Homo sapiens.
 OS Synthetic.

XX WO9839433-A1.

PD 11-SEP-1998.

PF 05-MAR-1998; 98WO-GB00727.

PR 05-MAR-1997; 97GB-0004519.

PA (ADPR-) ADPROTECH PLC.

PI Cox VF, Mossakowska DEL, Smith RAG;

DR WPI; 1998-506358/43.
 XX Soluble polypeptide comprising short consensus repeats from LHR-A -
 PT used to treat disorders and diseases associated with inflammation or
 PT inappropriate complement activation
 XX
 PS Claim 19; Page 55-56; 67pp; English.
 XX
 CC This is the amino acid sequence of CM16/cys5, a protein derived
 CC from CM15/cys (see W75989) with the modification IL24P (1.e.
 CC wild-type sequence at the hinge region between SCR2 and SCR3).
 CC CM15/cys consists of the short consensus repeats (SCR) 1-3 of the
 CC complement receptor type 1 (CRI) in which 23 amino acids have been
 CC substituted by those found at homologous positions of the CRI-like
 CC pseudogene sequence, plus an additional C-terminal cysteine residue.
 CC CM16/cys was expressed from plasmid pProcCRI-3CM16/cys in
 CC Escherichia coli, and was used in the construction of
 CC (CM16)-Cys-S-S-(MSWP-1) (see W75992). The invention provides novel
 CC soluble CRI-derived polypeptides (see W53236-47 and W75986-94) that
 CC act as complement inhibitors with functional complement inhibitory,
 CC including anti-haemolytic, activity. They are used to treat a
 CC disease or disorder associated with inflammation or inappropriate
 CC complement activation, such as neurological disorders (e.g.
 CC multiple sclerosis and Parkinson's disease), disorders of
 CC inappropriate or undesirable complement activation (e.g. xenograft
 CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,
 CC infection or sepsis, immune complex disorders and autoimmune
 CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and
 CC myasthenia gravis), and reproductive disorders.
 CC
 XX Sequence 198 AA;
 S0
 Query Match 95.1%; Score 1050; DB 19; Length 198;
 Best Local Similarity 93.9%; Pred. No. 4.1e-94;
 Matches 185; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MGNAPEMLEFARPTNLTDEFEPIGTLYNIECRPGYSGRPFSITCKNSWTGAKRCR 60
 DB 1 mgnvpewlpfarpnltdldfepigtlyniecrpgysgrpfslcknswtsakck 60
 QY 61 RKSCRNPDPVNGVMVAVIGIQSGSIKYSCTKGYRLIGSSSATCIIISGDTYVINDETPI 120
 DB 61 rkscrnpdpvngvmavikigiqsgsikysctkgyrllgsssatcillsdtyvindhktpv 120
 QY 121 CDRIPGGLPPTIANGDFTSISREFFHGSVVTYHNCNLSGSKKVFELVGEPSITCTSKD 180
 DB 121 cdripzglppliangdftsrsrefffhgsvvtynchnlsgskkvfelvgepsitctskd 180
 QY 181 QVGISGAPAPQCIIIPNK 197
 DB 181 qvgisgapapqcilipnk 197
 Db 181 qvgisgapapqcilipnk 197
 RESULT 12
 ID W75992
 W75992 standard; Protein: 215 AA.
 AC W75992;
 XX
 DT 18-JAN-1999 (first entry)
 XX
 DE (CM16)-Cys-S-S-(MSMAP-1) polypeptide.
 XX
 KW Complement receptor type-1; CRI; CM16; complement; inhibitor;
 KW myristoyl/electrostatic switch peptide reagent 1; MSWP-1;
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;
 KW xenograft rejection; inflammation; Crohn's disease; asthma;
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;
 KW myasthenia gravis; reproductive disorder; therapy.
 XX

OS Chimeric - Homo sapiens.
 OS Chimeric - Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..198
 FT Peptide /label= CM16/cys
 FT 199..215
 FT Disulfide-bond /label= MSWP-1
 FT Modified-site 199
 FT Modified-site 198..199
 FT Modified-site /note= "(S-2-thiopyridyl)cysteine"
 FT 215
 FT /note= "N-(myristoyl)-glycine"
 PN W09839433-A1.
 XX
 PD 11-SEP-1998.
 XX
 PF 05-MAR-1998; 98WO-GB00727.
 XX
 PR 05-MAR-1997; 97GB-0004519.
 XX
 PA (ADPR-) ADPROTECH PLC.
 XX
 PI COX VF, Mossakowska DEL, Smith RMG;
 XX
 DR WPI; 1998-506358/43.
 XX
 PT Soluble polypeptide comprising short consensus repeats from LHR-A -
 PT used to treat disorders and diseases associated with inflammation or
 PT inappropriate complement activation
 XX
 PS Claim 17; Page 56; 67pp; English.
 XX
 CC This is the amino acid sequence of (CM16)-Cys-S-S-(MSWP-1),
 CC comprising novel soluble complement receptor type 1 (CRI)-like
 CC polypeptide CM16 joined to a myristoyl/electrostatic switch peptide
 CC reagent 1 (MSWP-1). It was produced by coupling CM16/cys (see
 CC W75989) to a synthetic MSWP-1 peptide (see W75988). CM16 comprises
 CC the short consensus repeats (SCR) from CRI in which 23 amino acid
 CC residues are substituted by those corresponding to the CRI-like
 CC pseudogene. Soluble CRI-derived polypeptides of the invention (see
 CC W53236-47 and W75987-94) act as complement inhibitors with
 CC functional complement inhibitory, including anti-hemolytic,
 CC activity. These can be used to treat a disease or disorder
 CC associated with inflammation or inappropriate complement activation,
 CC such as neurological disorders (e.g. multiple sclerosis, Parkinson's
 CC disease), disorders of inappropriate or undesirable complement
 CC activation (e.g. xenograft rejection), inflammatory disorders (e.g.
 CC Crohn's disease, asthma, and acute pancreatitis), post-ischaemic
 CC reperfusion conditions, infection or sepsis, immune complex
 CC disorders and autoimmune diseases (e.g. rheumatoid arthritis,
 CC proliferative nephritis and myasthenia gravis), and reproductive
 CC disorders.
 CC
 XX Sequence 215 AA;
 S0
 Query Match 95.1%; Score 1050; DB 19; Length 215;
 Best Local Similarity 93.9%; Pred. No. 4.5e-94;
 Matches 185; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MGNAPEMLEFARPTNLTDEFEPIGTLYNIECRPGYSGRPFSITCKNSWTGANDRCR 60
 DB 1 mgnvpewlpfarpnltdldfepigtlyniecrpgysgrpfslcknswtsakck 60
 QY 61 RKSCRNPDPVNGVMVAVIGIQSGSIKYSCTKGYRLIGSSSATCIIISGDTYVINDETPI 120
 DB 61 rkscrnpdpvngvmavikigiqsgsikysctkgyrllgsssatcillsdtyvindhktpv 120
 QY 121 CDRIPGGLPPTIANGDFTSISREFFHGSVVTYHNCNLSGSKKVFELVGEPSITCTSKD 180
 DB 121 cdripzglppliangdftsrsrefffhgsvvtynchnlsgskkvfelvgepsitctskd 180
 Db 121 cdripzglppliangdftsrsrefffhgsvvtynchnlsgskkvfelvgepsitctskd 180

QY 1 MQCNAPEWLPFARPTNLDEFEFPIGTLYLNCRPGYSGRPFSSICLKNVWTGAKDRCR 60
 Db 1 mqcnapewlpfarptnldefeffigtylnyecrpygsrpfssiclknswtgkdr 60
 QY 61 RKSCRNPDPVNGMVHVTKGIQFGSQIKYSGTKGYRLIGSSATCIIISGDTYIMWNETPI 120
 Db 61 rkscrnpdpvngmvhvkigifgsqikysctkgyrllgssatcclisgdtvwdnetp 120
 QY 121 CDRIPCGLPPTIANGDEFNISREYFHGVSQVYTHCNLSRGKVFELVGEPSIYCTSKDD 180
 Db 121 cdrilpcglpplltngdfistnrenfhysvvtlyrcnpsggakvelfvgepsiyctsnd 180
 QY 181 QVGIWSGPAPQCIIPNK 197
 Db 181 qvgiwsgapqciipnk 197

RESULT 15
 W45909 standard; peptide; 211 AA.
 W45909;
 W45909;
 30-JUN-1998 (first entry)
 DE SCR 1-3 of complement receptor type 1 (CR1) derived protein.
 XX
 XX Membrane binding element; thrombotic disease; soluble protein;
 KW complement-related disease; integral membrane protein; inflammation;
 KM short consensus repeat; SCR 1-3; CR1; complement receptor type 1.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Cross-links 211
 FT /note= "Disulphide linked to Cys in peptide given
 FT in W45889"
 PN
 XX W09802454-A2.
 PD 22-JAN-1998.
 XX
 XX 08-JUL-1997; 97WO-EP03715.
 PF
 XX 15-JUL-1996; 96GB-0014871.
 PR
 XX (ADPR-) ADPROTECH PLC.
 PA
 XX Dodd I, Mossakowska DEI, Smith RAG;
 PI
 XX WPI: 1998-110524/10.
 DR
 XX
 XX Derivatives of soluble poly:peptide(s) bonded to low affinity
 PT membrane binding groups - useful for treating complement-related and
 PT thrombotic diseases, providing improved localisation at cellular
 PT membranes
 PS
 XX Claim 28; Page 65; 75pp; English.

This sequence is shown in the specification. The invention relates to a soluble derivative (A) of a soluble polypeptide (I), which comprises at least 2 heterologous membrane-binding elements (MBE) of low membrane affinity covalently associated with (I). MBE interact, independently and with thermodynamic additivity, with components of cellular or artificial membranes exposed to extracellular fluids. (A) are used to treat disorders treatable with (I) itself, specifically inflammation or any other complement-related disorder (e.g. neurological disease, graft rejection, myocardial infarction, sepsis, rheumatoid arthritis and many others; including application to indwelling devices) and thrombolytic disease, but also to treat allergy, induce weight loss, to treat ischemia or asthma and as immuno-modulators for treating multiple sclerosis. (A) are administered orally, topically, by injection or

CC Inhalation at 0.01-10 (preferably 0.1-10) mg/kg/day.
 XX
 SQ Sequence 211 AA;
 Query Match 94.8%; Score 1047; DB 19; Length 211;
 Best Local Similarity 94.9%; Pred. No. 8.6e-94;
 Matches 187; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MQCNAPEWLPFARPTNLDEFEFPIGTLYLNCRPGYSGRPFSSICLKNVWTGAKDRCR 60
 Db 1 mqcnapewlpfarptnldefeffigtylnyecrpygsrpfssiclknswtgkdr 60
 QY 61 RKSCRNPDPVNGMVHVTKGIQFGSQIKYSGTKGYRLIGSSATCIIISGDTYIMWNETPI 120
 Db 61 rkscrnpdpvngmvhvkigifgsqikysctkgyrllgssatcclisgdtvwdnetp 120
 QY 121 CDRIPCGLPPTIANGDEFNISREYFHGVSQVYTHCNLSRGKVFELVGEPSIYCTSKDD 180
 Db 121 cdrilpcglpplltngdfistnrenfhysvvtlyrcnpsggakvelfvgepsiyctsnd 180
 QY 181 QVGIWSGPAPQCIIPNK 197
 Db 181 qvgiwsgapqciipnk 197

Search completed: January 13, 2001, 13:42:31
 Job time: 3146 sec

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OM protein - protein search, using sw model

Run on: January 13, 2001, 13:09:15 ; Search time 27.14 Seconds

(without alignments)
130.344 Million cell updates/sec

Title: US-09-380-682-1

Perfect score: 1104

Sequence: 1 MOCNAPEMLPFARPNLTDEFEFFIGTYLNTYCRPGYSGRPSTICLNKSVTGAKDRCR

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Issued_Patents_AA: *
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6: /cgn2_6/ptodata/2/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1047	94.8	197	2	US-08-356-361-27
2	1047	94.8	197	2	US-08-769-967A-27
3	1047	94.8	254	2	US-08-356-361-29
4	1047	94.8	254	2	US-08-356-361-30
5	1047	94.8	254	2	US-08-769-967A-29
6	1047	94.8	254	2	US-08-769-967A-30
7	1042	94.4	1847	5	5256642-10
8	1042	94.4	1847	5	5256642-10
9	1042	94.4	2039	5	5256642-2
10	1042	94.4	2039	5	5472939-2
11	788	71.4	1466	5	5256642-6
12	788	71.4	1466	5	5472939-6
13	788	71.4	1537	5	5256642-5
14	788	71.4	1537	5	5472939-5
15	408	37.0	323	2	US-08-435-149-2
16	408	37.0	324	1	US-08-310-416A-14
17	408	37.0	324	2	US-08-888-171-14
18	408	37.0	577	2	US-08-435-149-3
19	361	32.7	76	2	US-08-356-361-28
20	361	32.7	76	2	US-08-769-967A-28
21	361	32.7	133	2	US-08-356-361-31
22	361	32.7	133	2	US-08-769-967A-31
23	346	31.3	60	1	US-08-210-266A-10
24	346	31.3	60	1	US-08-688-675-10
25	346	31.3	60	3	US-08-477-860C-10
26	340	30.8	62	1	US-08-210-266A-12
27	340	30.8	62	1	US-08-688-675-12
28	340	30.8	62	3	US-08-477-860C-12

29	295	26.7	254	1	US-08-310-416A-13	Sequence 13, Appl
30	295	26.7	254	2	US-08-888-171-13	Sequence 13, Appl
31	295	26.7	254	2	US-08-435-149-1	Sequence 1, Appl
32	295	26.7	293	2	US-08-310-416A-16	Sequence 16, Appl
33	295	26.7	293	2	US-08-888-171-16	Sequence 16, Appl
34	295	26.7	324	2	US-08-528-057-46	Sequence 46, Appl
35	295	26.7	370	2	US-08-528-057-42	Sequence 42, Appl
36	295	26.7	373	2	US-08-528-057-44	Sequence 44, Appl
37	295	26.7	377	2	US-08-528-057-2	Sequence 2, Appl
38	295	26.7	384	5	5514787-2	Sequence 2, Appl
39	288.5	26.1	263	1	US-07-906-983-2	Patent No. 5514787
40	270.5	24.5	128	5	5514582-42	Sequence No. 5514582
41	243.5	22.1	126	5	5514582-43	Patent No. 5514582
42	229	20.7	62	1	US-08-210-266A-13	Sequence 13, Appl
43	229	20.7	62	1	US-08-688-675-13	Sequence 13, Appl
44	229	20.7	62	3	US-08-477-860C-13	Sequence 13, Appl
45	197	17.8	290	3	US-08-824-692-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-356-361-27
Sequence 27, Application US/08356361
Patent No. 5833989
GENERAL INFORMATION:
APPLICANT: Smith, Richard A.G.
APPLICANT: Dodd, Ian
APPLICANT: Freeman Mary A.
APPLICANT: Mossakowska, Danuta E.I.
TITLE OF INVENTION: No. 5833989e1 Compounds
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham-Corporate Intellectual Property
STREET: P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,361
FILING DATE: 03-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jervys, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P30423
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-356-361-27

Query Match 94.8% Score 1047; DB 2; Length 197;
Best Local Similarity 94.98; Pred. No. 1.2e-103;
Matches 187; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
DB 1 MOCNAPEMLPFARPNLTDEFEFFIGTYLNTYCRPGYSGRPSTICLNKSVTGAKDRCR 60
|||||
1 MOCNAPEMLPFARPNLTDEFEFFIGTYLNTYCRPGYSGRPSTICLNKSVTGAKDRCR 60

Qy	61	RKSGRNPPDPVNGAVHVIKIGIOFSQAKYTSOTKCYRLIGSSASACIIISGDTVIMDNETPI	120
Dd	61	RKSGRNPPDPVNGAVHVIKIGIOFSQAKYTSOTKCYRLIGSSASACIIISGDTVIMDNETPI	120
Qy	121	CDRIIPCGIPPIIANGDPTSIISREYFHGVSVTYTCNIGSGKRYEELVGPSPSTYCSKDD	180
Dd	121	CDRIIPCGIPPIIANGDPTSIISREYFHGVSVTYTCNIGSGKRYEELVGPSPSTYCSKDD	180
Qy	181	QVGIMSGPAPDCIIIPNK	197
Dd	181	QVGIMSGPAPDCIIIPNK	197

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1      RESULT      2
2      US-08-769-967A-27
3      : Sequence 27, Application US/08769967A
4      : Patent No. 5859223
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Mossakowska, Danuta E.I.
9      : APPLICANT: Smith, Richard A.G.
10     : APPLICANT: Dodd, Ian
11     : APPLICANT: Freeman, Anne Mary
12     : TITLE OF INVENTION: Soluble CRI Derivatives
13     :
14     : NUMBER OF SEQUENCES: 33
15     :
16     : CORRESPONDENCE ADDRESS:
17     : ADDRESSEE: SmithKline Beecham Corporate Intellectual Property
18     : STREET: P.O. Box 1539
19     : CITY: King of Prussia
20     : STATE: Pennsylvania
21     : COUNTRY: USA
22     :
23     : ZIP: 19406
24     :
25     : COMPUTER READABLE FORM:
26     :
27     : MEDIUM TYPE: Floppy disk
28     : COMPUTER: IBM PC compatible
29     : OPERATING SYSTEM: PC-DOS/MS-DOS
30     : SOFTWARE: Patent In Release #1.0, Version #1.25
31     :
32     : CURRENT APPLICATION DATA:
33     : APPLICATION NUMBER: US/08/769,967A
34     : FILING DATE:
35     : CLASSIFICATION: 536
36     : PRIOR APPLICATION DATA:
37     : APPLICATION NUMBER: 08/440,569
38     : FILING DATE: 15-May-1995
39     : ATTORNEY/AGENT INFORMATION:
40     : NAME: King, William T.
41     : REGISTRATION NUMBER: 30,954
42     : REFERENCE/DOCKET NUMBER: P30423C2
43     : TELECOMMUNICATION INFORMATION:
44     : TELEPHONE: (610) 270-5364
45     : TELEFAX: (610) 270-5090
46     : INFORMATION FOR SEQ ID NO: 27:
47     :
48     : SEQUENCE CHARACTERISTICS:
49     : LENGTH: 197 amino acids
50     : TYPE: amino acid
51     : TOPOLOGY: linear
52     :
53     : MOLECULE TYPE: peptide
54     : FRAGMENT TYPE: N-terminal
55     :
56     : US-08-769-967A-27

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Query Match	94.8%	Score 1047	DB 2	Length 197
Best Local Similarity	94.9%	Pred. No. 1,2e-103		
Matches 187	Conservative	2	Mismatches 8	Indels 0
			Gaps 0	
QY	1	MCCNAPEWLPFRPTNLTDGEFFPIGTLYNTECRPEYSGRPSIITLKNQSVMTGAKDRCR	60	
DB	1	MCCNAPEWLPFRPTNLTDGEFFPIGTLYNTECRPEYSGRPSIITLKNQSVMTGAKDRCR	60	
OY	61	RKRCRNPDPVNGMVAVIRIGIOGSGIRKSCITGXYLTISSSATTCTIISDPTIYMNDEETPI	120	
DB	61	RKRCRNPDPVNGMVAVIRIGIOGSGIRKSCITGXYLTISSSATTCTIISDPTIYMNDEETPI	120	

[illegible]

RESULT 3
 US-08-356-361-29
 Sequence 29, Application US/08356361
 Patent No. 5833989
 GENERAL INFORMATION:
 APPLICANT: Smith, Richard A.G.
 APPLICANT: Dodd, Ian
 APPLICANT: Freeman Mary A.
 APPLICANT: Mosakowska, Danuta E.I.
 TITLE OF INVENTION: No. 5833989el Compounds
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Smltkline Beecham-Corporate Intellectual Property
 STREET: P.O. Box 1539
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19406
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/356,361
 FILING DATE: 03-Jul-1995
 CLASSIFICATION: 433
 ATTORNEY/AGENT INFORMATION:
 NAME: Jervis, Herbert H.
 REGISTRATION NUMBER: 31,171
 REFERENCE/DOCKET NUMBER: P30423
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 270-5019
 TELEFAX: (610) 270-5050
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 254 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: N-terminal
 US-08-356-361-29

	Query Match	Similarity	94.8%	Score 1047	DB 2:	Length 254:
	Best Local	Similarity	94.9%	Pred. No. 1,76-103:		
	Matches 187:	Conservative	2:	Mismatches 8:	Indels 0:	Gaps 0:
QY	1	MQCNAPPEMLPEARPNLIDEEFFPIGTYLNECRPGYSGRPESITCLNKSWTGAKDCR	60			
Db	1	MQCNAPPEMLPEARPNLIDEEFFPIGTYLNECRPGYSGRPESITCLNKSWTGAKDCR	60			
QY	61	RKSCANPPDPVNGMHHVKGIOFSQIYSCTKGYRLIGSSATCIIIGDPYIMNENPI	120			
Db	61	RKSCANPPDPVNGMHHVKGIOFSQIYSCTKGYRLIGSSATCIIIGDPYIMNENPI	120			
QY	121	CRIFCGLPPTIANDDEFTSISREYHSGSVYVYHCLNLSRGKRVELVGEPSIYCTSKDD	180			
Db	121	CRIFCGLPPTIANDDEFTSISREYHSGSVYVYHCLNLSRGKRVELVGEPSIYCTSKDD	180			
QY	181	QVGIWSGPAPOCIIIPNK	197			
Db	181	QVGIWSGPAPOCIIIPNK	197			

RESULT 4
US-08-356-361-30
; Sequence 30, Application US/08356361
; Patent No. 5833989
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard A.G.
; APPLICANT: Dodd, Ian
; APPLICANT: Freeman Mary A.
; APPLICANT: Mossakowska, Danuta E.I.
; TITLE OF INVENTION: No. 5833989el Compounds
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham-Corporate Intellectual Property
; STREET: P.O. Box 1539
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,361
; FILING DATE: 03-Jul-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jervls, Herbert H.
; REGISTRATION NUMBER: 31,171
; REFERENCE/DOCKET NUMBER: P30423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5019
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-356-361-30

Query Match 94.8%; Score 1047; DB 2; Length 254;
Best Local Similarity 94.9%; Pred. No. 1.7e-103;
Matches 187; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
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DB 1 MOCNAPBMLPFARPTNLTDEFFPIGTYLYNECRPGYSGRPFSLICLKNVMTGAKDRCR 60
QY 61 RKSCRNPDPVNGVNHVYIKIQGSOIKYSCITGKRGRLIGSSSATCIIISGDTIVMDNETPI 120
DB 61 RKSCRNPDPVNGVNHVYIKIQGSOIKYSCITGKRGRLIGSSSATCIIISGDTIVMDNETPI 120
QY 121 CDRIPGCLPPTIANGDFTSISREYFHYGVYTYHCNLSRGKVFELVGPESIVCTSKDD 180
DB 121 CDRIPGCLPPTIANGDFTSISREYFHYGVYTYHCNLSRGKVFELVGPESIVCTSKDD 180
QY 181 QVGIMSGPAPCIIIPNK 197
DB 181 QVGIMSGPAPCIIIPNK 197

RESULT 5
US-08-769-967A-29
; Sequence 29, Application US/08769967A
; Patent No. 5859223
; GENERAL INFORMATION:
; APPLICANT: Mossakowska, Danuta E.I.
; APPLICANT: Smith, Richard A.G.

APPLICANT: Dodd, Ian
APPLICANT: Freeman, Anne Mary
TITLE OF INVENTION: Soluble CRI Derivatives
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporate Intellectual Property
STREET: P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,967A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/440,569
FILING DATE: 15-May-1995
ATTORNEY/AGENT INFORMATION:
NAME: KING, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: P30423C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5364
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-769-967A-29

Query Match 94.8%; Score 1047; DB 2; Length 254;
Best Local Similarity 94.9%; Pred. No. 1.7e-103;
Matches 187; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 MOCNAPBMLPFARPTNLTDEFFPIGTYLYNECRPGYSGRPFSLICLKNVMTGAKDRCR 60
DB 1 MOCNAPBMLPFARPTNLTDEFFPIGTYLYNECRPGYSGRPFSLICLKNVMTGAKDRCR 60
QY 61 RKSCRNPDPVNGVNHVYIKIQGSOIKYSCITGKRGRLIGSSSATCIIISGDTIVMDNETPI 120
DB 61 RKSCRNPDPVNGVNHVYIKIQGSOIKYSCITGKRGRLIGSSSATCIIISGDTIVMDNETPI 120
QY 121 CDRIPGCLPPTIANGDFTSISREYFHYGVYTYHCNLSRGKVFELVGPESIVCTSKDD 180
DB 121 CDRIPGCLPPTIANGDFTSISREYFHYGVYTYHCNLSRGKVFELVGPESIVCTSKDD 180
QY 181 QVGIMSGPAPCIIIPNK 197
DB 181 QVGIMSGPAPCIIIPNK 197

RESULT 6
US-08-769-967A-30
; Sequence 30, Application US/08769967A
; Patent No. 5859223
; GENERAL INFORMATION:
; APPLICANT: Mossakowska, Danuta E.I.
; APPLICANT: Smith, Richard A.G.
; APPLICANT: Dodd, Ian
; APPLICANT: Freeman, Anne Mary
; TITLE OF INVENTION: Soluble CRI Derivatives
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporate Intellectual Property
STREET: P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,967A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/440,569
FILING DATE: 15-May-1995
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: P30423C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5364
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-769-967A-30

Query Match 94.8%; Score 1047; DB 2; Length 254;
Best Local Similarity 94.9%; Pred. No. 1.7e-103;
Matches 187; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MOCNAPEWLPFARPTNLDEFEFPITGYLNECRPGYSGRPSIILKNSVWTGAKRDR 60
DB 1 MOCNAPEWLPFARPTNLDEFEFPITGYLNECRPGYSGRPSIILKNSVWTGAKRDR 60
QY 61 RKSCHNPDPVNGMVHVIKIOFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPFI 120
DB 61 RKSCHNPDPVNGMVHVIKIOFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPFI 120
QY 121 CRIPGCLPPTIANGDFTSISREYFHGVSVYTYHCLNLSGKRVFELVGEPSIYCTSKDD 180
DB 121 CRIPGCLPPTIANGDFTSISREYFHGVSVYTYHCLNLSGKRVFELVGEPSIYCTSKDD 180
QY 181 QVGWGPAPQCIIPNK 197
DB 181 QVGWGPAPQCIIPNK 197

RESULT 7
5256642-10
Patent No. 5256642
APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
RECEPTOR 1 (CRI) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
USE THEREOF
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,128
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865

FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO: 10;
LENGTH: 1847
5256642-10

Query Match 94.4%; Score 1042; DB 5; Length 1847;
Best Local Similarity 94.9%; Pred. No. 8.6e-102;
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNAPFWLPFARPTNLDEFEFPITGYLNECRPGYSGRPSIILKNSVWTGAKRDR 61
DB 47 QCNAPFWLPFARPTNLDEFEFPITGYLNECRPGYSGRPSIILKNSVWTGAKRDR 106
QY 62 KSCRNPPDPVNGMVHVIKIOFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPFI 121
DB 107 KSCRNPPDPVNGMVHVIKIOFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPFI 166
QY 122 DRIPGCLPPTIANGDFTSISREYFHGVSVYTYHCLNLSGKRVFELVGEPSIYCTSKDD 181
DB 167 DRIPGCLPPTIANGDFTSISREYFHGVSVYTYHCLNLSGKRVFELVGEPSIYCTSKDD 226
QY 182 VGIWGPAPQCIIPNK 197
DB 227 VGIWGPAPQCIIPNK 242

RESULT 8
5472939-10
Patent No. 5472939

APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
MEDIATED DISORDERS
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,825
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588,128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO: 10;
LENGTH: 2006
5472939-10

Query Match 94.4%; Score 1042; DB 5; Length 1847;
Best Local Similarity 94.9%; Pred. No. 8.6e-102;
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNAPFWLPFARPTNLDEFEFPITGYLNECRPGYSGRPSIILKNSVWTGAKRDR 61
DB 47 QCNAPFWLPFARPTNLDEFEFPITGYLNECRPGYSGRPSIILKNSVWTGAKRDR 106
QY 62 KSCRNPPDPVNGMVHVIKIOFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPFI 121
DB 107 KSCRNPPDPVNGMVHVIKIOFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPFI 166
QY 122 DRIPGCLPPTIANGDFTSISREYFHGVSVYTYHCLNLSGKRVFELVGEPSIYCTSKDD 181
DB 167 DRIPGCLPPTIANGDFTSISREYFHGVSVYTYHCLNLSGKRVFELVGEPSIYCTSKDD 226
QY 182 VGIWGPAPQCIIPNK 197

Db 227 VGIMSGPAPQCIIPNK 242

RESULT 9

5256642-2

Patent No. 5256642

APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
RECEPTOR 1 (CR1) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
USE THEREOF

NUMBER OF SEQUENCES: 30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/588,128

FILING DATE: 24-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 412,745

FILING DATE: 26-SEP-1989

APPLICATION NUMBER: 332,865

FILING DATE: 03-APR-1989

APPLICATION NUMBER: 176,532

FILING DATE: 01-APR-1988

SEQ ID NO: 2:

LENGTH: 2039

5256642-2

Query Match

Best Local Similarity 94.4%; Score 1042; DB 5; Length 2039;
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNAPENLPFARPTNLTDEEFPPIGTYLNECRPGYSGRPFSTICLNKSNVTGAKDRCR 61

DB 42 QCNAPENLPFARPTNLTDEEFPPIGTYLNECRPGYSGRPFSTICLNKSNVTGAKDRCR 101

QY 62 KSCRNPDPVNGVHVYKIOFGSQIKYCTKGRYLRIGSSSACIIISGDIYVNDNEPIC 121

DB 102 KSCRNPDPVNGVHVYKIOFGSQIKYCTKGRYLRIGSSSACIIISGDIYVNDNEPIC 161

QY 122 DRIPCGLPPTIANGDFTSISREYFHGVSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 181

DB 162 DRIPCGLPPTIANGDFTSISREYFHGVSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 221

QY 182 VGIMSGPAPQCIIPNK 197

DB 222 VGIMSGPAPQCIIPNK 237

RESULT 10

5472939-2

Patent No. 5472939

APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
MEDICATED DISORDERS

NUMBER OF SEQUENCES: 30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/138,825

FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 588,128

FILING DATE: 24-SEP-1990

APPLICATION NUMBER: 412,745

FILING DATE: 26-SEP-1989

APPLICATION NUMBER: 332,865

FILING DATE: 03-APR-1989

APPLICATION NUMBER: 176,532

FILING DATE: 01-APR-1988

SEQ ID NO: 2:

LENGTH: 2039

5472939-2

Query Match

Best Local Similarity 94.4%; Score 1042; DB 5; Length 2039;
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNAPENLPFARPTNLTDEEFPPIGTYLNECRPGYSGRPFSTICLNKSNVTGAKDRCR 61

DB 42 QCNAPENLPFARPTNLTDEEFPPIGTYLNECRPGYSGRPFSTICLNKSNVTGAKDRCR 101

QY 62 KSCRNPDPVNGVHVYKIOFGSQIKYCTKGRYLRIGSSSACIIISGDIYVNDNEPIC 121

DB 102 KSCRNPDPVNGVHVYKIOFGSQIKYCTKGRYLRIGSSSACIIISGDIYVNDNEPIC 161

QY 122 DRIPCGLPPTIANGDFTSISREYFHGVSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 181

DB 162 DRIPCGLPPTIANGDFTSISREYFHGVSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 221

QY 182 VGIMSGPAPQCIIPNK 197

DB 222 VGIMSGPAPQCIIPNK 237

RESULT 11

5256642-6

Patent No. 5256642

APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
RECEPTOR 1 (CR1) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
USE THEREOF

NUMBER OF SEQUENCES: 30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/588,128

FILING DATE: 24-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 412,745

FILING DATE: 26-SEP-1989

APPLICATION NUMBER: 332,865

FILING DATE: 03-APR-1989

APPLICATION NUMBER: 176,532

FILING DATE: 01-APR-1988

SEQ ID NO: 6:

LENGTH: 1466

5256642-6

Query Match

Best Local Similarity 71.4%; Score 788; DB 5; Length 1466;
Matches 142; Conservative 14; Mismatches 39; Indels 0; Gaps 0;

QY 3 CNAPENLPFARPTNLTDEEFPPIGTYLNECRPGYSGRPFSTICLNKSNVTGAKDRCR 62

DB 441 QCNAPENLPFARPTNLTQNASDPPIGTSIKYCRPEYIGRPSICLDLWVSSPDVCKRK 500

QY 63 SCRNPDPVNGVHVYKIOFGSQIKYCTKGRYLRIGSSSACIIISGDIYVNDNEPIC 122

DB 501 SCRNPDPVNGVHVYKIOFGSQIKYCTKGRYLRIGSSSACIIISGDIYVNDNEPIC 560

QY 123 RIPCGLPPTIANGDFTSISREYFHGVSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 182

DB 561 RIPCGLPPTIANGDFTSISREYFHGVSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 620

QY 183 GIMSGPAPQCIIPNK 197

DB 621 GIMSGPAPQCIIPNK 635

RESULT 12

5472939-6

Patent No. 5472939

APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,

```

MINNIE W.;CARSON, GERALD R.;CONCINO, MICHAEL F.;JP, STEPHEN
H.;MARRIDES, SAVVAS;MARSH, HENRY C. JR.
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
MEDATED DISORDERS
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138, 825
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588, 128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412, 745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332, 865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176, 532
FILING DATE: 01-APR-1988
SEQ ID NO:5:
LENGTH: 1466
5472939-6

Query Match 71.4%; Score 788; DB 5; Length 1466;
Best Local Similarity 72.8%; Pred. No. 5.8e-75;
Matches 142; Conservative 14; Mismatches 39; Indels 0; Gaps 0;

QY 3 CNAPEWLFARPTNLTDEFEPIGYLYNTECRPGYSGRPSTICLKNVWTGAKDRCK 62
DB 441 CQAPDHFFFAKLTQTNASDFIGTSLKRECPREYXGRFSTICDNLVWSSPKDVKRK 500
QY 63 SCRNPPDDVNGVHVHVIKQIFGSOIKYCTGKRYLIGSSAACIIISGDIYVINDNETPICD 122
DB 501 SCRTPPDDVNGVHVHVIKQIFGSOIKYCTGKRYLIGSSAACIIISGDIYVINDNETPICD 560
QY 123 RIPCGLPTIANGDTSISREYFHGYSVVTYHCNLGSRCKKVFELVGEPSIYCTSKDDY 182
DB 561 RIPCGLPTIANGDTSISREYFHGYSVVTYHCNLGSRCKKVFELVGEPSIYCTSKDDY 620
QY 183 GIWGPAPQCIIPNK 197
DB 621 GIWGPAPQCIIPNK 635

RESULT 13
5256642-5
Patent No. 5256642
APPLICANT: FEARON, DOUGLAS T.;KLICKSTEIN, LLOYD B.;WONG,
MINNIE W.;CARSON, GERALD R.;CONCINO, MICHAEL F.;JP, STEPHEN
H.;MARRIDES, SAVVAS;MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
RECEPTOR 1 (CRL) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
USE THEREOF
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,128
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412, 745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332, 865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176, 532
FILING DATE: 01-APR-1988
SEQ ID NO:5:
LENGTH: 1537
5256642-5

Query Match 71.4%; Score 788; DB 5; Length 1537;
Best Local Similarity 72.8%; Pred. No. 6.1e-75;
Matches 142; Conservative 14; Mismatches 39; Indels 0; Gaps 0;

QY 3 CNAPEWLFARPTNLTDEFEPIGYLYNTECRPGYSGRPSTICLKNVWTGAKDRCK 62

```

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Db 441 CQAPDHLFLAKLTQTNASDPIGSLKYECPREYGRPSISICLDNLVWSSPKDVCRRK 500
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 SCRNPPDPVNGVAVHIKIKIOFGSOLIKYSCIRKGYELIGSSATCIIISGDTYIMDNERPICD 122
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 501 SCTPPDPVNGVAVHITDIOVGSRLNYSCTGHRILGHSSAECLISGNTAHMSTKPPICQ 560
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 123 RIPCGLPPIANGDPTISISREYFHGSVVYTHCNLMGSRKAKVELYGEPSIYCTSKDDQV 182
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 561 RIPCGLPPIANGDPTISINRENHFHGSVYVYRCNLMGSRKAKVELYGEPSIYCTSNDDQV 620
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QY 183 GWSGPAPOCIIIPNK 197
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Db 621 GWSGPAPOCIIIPNK 635
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RESULT 14
5472939-5
; Patent No. 5472939
; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; TP, STEPHEN
; H.; MARRIDES, SAVVAS; MARSH, HENRY C. JR.
; TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
; MEDIATED DISORDERS
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138,825
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 588,128
; FILING DATE: 24-SEP-1990
; APPLICATION NUMBER: 412,745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332,865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176,532
; FILING DATE: 01-APR-1988
; SEQ ID NO:5
; LENGTH: 1537
5472939-5

Query Match 71.4%; Score 788; Db 5; Length 1537;
Best Local Similarity 72.8%; Pred. No. 6,1e-75;
Matches 142; Conservative 14; Mismatches 39; Indels 0; Gaps 0

QY 3 CNAPEMLPFRARPPLNLDFEEFPIGTYLNECPKPGISGSPBSITCLKKSQWTGANDRCRRK 62
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Db 441 CQAPDHLFLAKLTQTNASDPIGSLKYECPREYGRPSISICLDNLVWSSPKDVCRRK 500
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 SCRNPPDPVNGVAVHIKIKIOFGSOLIKYSCIRKGYELIGSSATCIIISGDTYIMDNERPICD 122
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 501 SCTPPDPVNGVAVHITDIOVGSRLNYSCTGHRILGHSSAECLISGNTAHMSTKPPICQ 560
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 123 RIPCGLPPIANGDPTISISREYFHGSVVYTHCNLMGSRKAKVELYGEPSIYCTSKDDQV 182
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 561 RIPCGLPPIANGDPTISINRENHFHGSVYVYRCNLMGSRKAKVELYGEPSIYCTSNDDQV 620
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 GWSGPAPOCIIIPNK 197
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 621 GWSGPAPOCIIIPNK 635
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RESULT 15
US-08-435-149-2
; Sequence 2, Application US/08435149
; Patent No. 5866402
; GENERAL INFORMATION:
; APPLICANT: INNIS, MICHAEL A.
; APPLICANT: ZAROR, ISABEL
; APPLICANT: CREASEY, ABILA A.
; TITLE OF INVENTION: CHIMERIC MCP AND DAF PROTEINS WITH CELL
; TITLE OF INVENTION: SURFACE LOCALIZING DOMAIN

```

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CITRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
CITY: EMERYVILLE
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,149
FILING DATE: 05-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SAVERIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0989.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-435-149-2

Query Match 37.0%; Score 408; DB 2; Length 323;
Best Local Similarity 42.6%; Pred. No. 1.6e-35;
Matches 83; Conservative 29; Mismatches 69; Indels 14; Gaps 6;

QY 3 CNAPMLPFA--RPTNLDEFEFPIGTLYNFCRPGYSGRPF--SIICLKNSVWTGARD 57
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Db 64 CEVPTRLNLSIKOPITQNY-FPVGTVEYECRPGYRREPSLSPKLTCLQNLKMTAVE 122
| | | | | : | | | | | | | | | | : | | | | :
QY 58 RCRRKSCRRPPVNCMVAVIKIGIOGSIKYSCTKGYRLIGSSSATCIISGDTVIMDNE 117
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| | | | | : | | | | | | | | | | : | | | | :
QY 118 TPICDRIPCGLPPTIANGDFTSISREYFHGVSVTYHNCNLGSRGKKVFELVGPSTICTS 177
| | | | | : | | | | | | | | | | : | | | | :
Db 183 LPECREIYCPAPQIDNGIIOG-ERDHYGYROSVTYACNKG-----FTWIGEHSLICTV 235
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QY 178 KDOVGWMSGAPAPQC 192
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Db 236 NNDE-GEWMSGPPEEC 249
| | | | | : | | | | | : | | | | | :

Search completed: January 13, 2001, 13:43:11
Job time: 2036 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2001, 13:10:30 ; Search time 72.05 Seconds
(without alignments)
185.655 Million cell updates/sec

Title: US-09-380-682-1
Perfect score: 1104

Sequence: 1 MGNAPWLPFARPTNLDE.....KDOVGIMSGPAPOCITPNK 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR66:*

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1042	94.4	2489	2	I73012 complement C3b/C4b
2	1038	94.0	482	2	A34924 complement C3b/C4b
3	1029	93.2	2014	2	I36936 complement recepto
4	702	63.6	440	2	A43519 complement recepto
5	699	63.3	433	2	A30550 complement C3b/C4b
6	689	62.4	497	2	UC2054 complement regulat
7	674	56.5	676	2	A45900 complement C3b rec
8	474	42.9	330	2	I55975 X/Y protein - mous
9	408	37.0	381	1	B26359 decay-accelerating
10	408	37.0	440	2	A62659 decay-accelerating
11	404	36.6	340	2	I56234 decay-accelerating
12	370.5	33.6	558	2	S57953 decay-accelerating
13	366	33.2	211	2	A46458 human CRI homolog
14	364.5	33.0	610	1	I46001 C4b-binding protei
15	359.5	32.6	597	1	S53711 C4BP alpha chain p
16	342.5	31.0	579	2	A56740 sperm-egg recognit
17	335.5	30.4	1025	1	A43526 complement C3d/Eps
18	325.5	29.5	469	1	NBMS4 C4b-binding protei
19	315.5	28.6	597	1	NBHU4 C4b-binding protei
20	295	26.7	349	2	G02913 sperm CD46 - human
21	295	26.7	369	2	I57998 membrane cofactor
22	295	26.7	377	2	I54479 membrane cofactor
23	295	26.7	384	2	S01896 membrane cofactor
24	292	26.4	302	1	MMBIE secretory compleme
25	292	26.4	360	1	MMBIE2E membrane-bound com
26	290	26.3	156	2	B30550 complement C3b/C4b
27	290	26.3	360	2	T42921 complement control
28	288.5	26.1	263	1	MMVZSP apolipoprotein H h
29	286.5	26.0	362	2	JC5194 membrane cofactor

30	286.5	26.0	369	2	JC5138 membrane cofactor
31	284.5	25.8	263	1	C36838 complement control
32	282.5	25.6	263	2	B72152 B18l protein - var
33	282.5	25.6	263	2	T28450 hypothetical prote
34	281	25.5	1091	1	PI0009 complement C3d/Eps
35	251	22.7	1234	1	NBMSH complement factor
36	234.5	21.2	449	1	NBRUHS complement factor
37	234.5	21.2	1231	1	NBRUH complement factor
38	229	20.7	560	2	T16833 hypothetical factor
39	222.5	20.2	363	2	B45900 complement C3d/Eps
40	222.5	20.2	1053	2	S46199 probable complemen
41	212	19.2	768	2	A42755 P-selectin precurs
42	212	19.2	768	2	I53821 P-selectin - rat
43	211.5	18.2	830	2	T20239 P-selectin prote
44	188.5	17.1	830	2	A30359 P-selectin - pig
45	187.5	17.0	482	2	JC5092

ALIGNMENTS

RESULT 1
I73012
complement C3b/C4b receptor, membrane-bound form precursor - human
N:Alternate names: Complement C3b/C4b receptor; complement receptor type 1 (CRI); sur
N:Contains: Complement C3b/C4b receptor, secreted form
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence revision 24-Nov-1999 #text change 21-Jul-2000
C:Accession: I73012; I56203; A47602; S03291; S03843; A28507; A24748; C24748
R:Yik, D.P.; Wong, W.W.
J. Immunol. 151, 6214-6224, 1993
A:Reference number: I56203; MUID:94065175
A:Accession: I73012
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Title: Structure of the gene for the F allele of complement receptor type 1 and seq
A:Reference number: I56203; MUID:94065175
A:Accession: I73012
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-683, 'X', 685-894, 'A', 896-1000, 1451-1471, 'X', 1473-2489 <VIK1>
A:Cross-references: GB:LI7418; NID:9306678; PIDN:AAB60695.1; PID:9451303
A:Accession: I56203
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-41 <MON>
A:Cross-references: GB:X14893
R:Wong, W.W.; Cahill, J.M.; Rosen, M.D.; Kennedy, C.A.; Bonaccio, E.T.; Morris, M.J.;
J. Exp. Med. 169, 847-863, 1989
A:Title: Structure of the human CRI gene. Molecular basis of the structural and quant
A:Reference number: A47602; MUID:89176869
A:Accession: A47602
A:Molecule type: DNA
A:Residues: 1-41 <MON>
A:Cross-references: GB:X14893
R:Hourcade, D.; Miesner, D.R.; Atkinson, J.P.; Holers, V.M.
J. Exp. Med. 168, 1255-1270, 1988
A:Title: Identification of an alternative polyadenylation site in the human C3b/C4b r
type 1.
A:Reference number: S03291; MUID:89010527
A:Accession: S03291
A:Molecule type: mRNA
A:Residues: 26-584 <HOV>
A:Cross-references: EMBL:X14362; NID:930197; PIDN:CAA3241.1; PID:g736240
R:Experimental source: Clone CRI-4
R:Klickstein, L.B.; Bartow, T.J.; Miletic, V.; Rabson, L.D.; Smith, J.A.; Fearon, D.T
J. Exp. Med. 168, 1699-1717, 1988
A:Title: Identification of distinct C3b and C4b recognition sites in the human C3b/C4
A:Reference number: S03843; MUID:89035592
A:Accession: S03843
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-894, 'A', 896-1000, 1451-2064, 'I', 2066-2276, 'P', 2278-2299, 'H', 2301-2325, 'T
R:Cross-references: EMBL:Y00816; NID:930185; PIDN:CAAB6875.1; PID:g30186
R:Klickstein, L.B.; Wong, W.W.; Smith, J.A.; Weiss, J.H.; Wilson, J.G.; Fearon, D.T.
J. Exp. Med. 165, 1095-1112, 1987
A:Title: Human C3b/C4b receptor (CRI). Demonstration of long homologous repeating dom

A:Reference number: A28507; MUID:87168191
A:Accession: A28507
A:Molecule type: mRNA
A:Residues: 933-1221, 'FV',1224-2064, 'I', 2066-2276, 'P', 2278-2299, 'H', 2301-2325, 'T', 2327-2342, 'G', 2344-2359, 'A', 2361-2376, 'C', 2378-2393, 'G', 2395-2410, 'A', 2412-2427, 'G', 2429-2444, 'A', 2446-2461, 'G', 2463-2478, 'A', 2480-2495, 'G', 2497-2512, 'A', 2514-2529, 'G', 2531-2546, 'A', 2548-2563, 'G', 2565-2580, 'A', 2582-2597, 'G', 2599-2614, 'A', 2616-2631, 'G', 2633-2648, 'A', 2650-2665, 'G', 2667-2682, 'A', 2684-2699, 'G', 2701-2716, 'A', 2718-2733, 'G', 2735-2750, 'A', 2752-2767, 'G', 2769-2784, 'A', 2786-2801, 'G', 2803-2818, 'A', 2820-2835, 'G', 2837-2852, 'A', 2854-2869, 'G', 2871-2886, 'A', 2888-2903, 'G', 2905-2920, 'A', 2922-2937, 'G', 2939-2954, 'A', 2956-2971, 'G', 2973-2988, 'A', 2990-3005, 'G', 3007-3022, 'A', 3024-3039, 'G', 3041-3056, 'A', 3058-3073, 'G', 3075-3090, 'A', 3092-3107, 'G', 3109-3124, 'A', 3126-3141, 'G', 3143-3158, 'A', 3160-3175, 'G', 3177-3192, 'A', 3194-3209, 'G', 3211-3226, 'A', 3228-3243, 'G', 3245-3260, 'A', 3262-3277, 'G', 3279-3294, 'A', 3296-3311, 'G', 3313-3328, 'A', 3330-3345, 'G', 3347-3362, 'A', 3364-3379, 'G', 3381-3396, 'A', 3398-3413, 'G', 3415-3430, 'A', 3432-3447, 'G', 3449-3464, 'A', 3466-3481, 'G', 3483-3498, 'A', 3500-3515, 'G', 3517-3532, 'A', 3534-3549, 'G', 3551-3566, 'A', 3568-3583, 'G', 3585-3600, 'A', 3602-3617, 'G', 3619-3634, 'A', 3636-3651, 'G', 3653-3668, 'A', 3670-3685, 'G', 3687-3702, 'A', 3704-3719, 'G', 3721-3736, 'A', 3738-3753, 'G', 3755-3770, 'A', 3772-3787, 'G', 3789-3804, 'A', 3806-3821, 'G', 3823-3838, 'A', 3840-3855, 'G', 3857-3872, 'A', 3874-3889, 'G', 3891-3906, 'A', 3908-3923, 'G', 3925-3940, 'A', 3942-3957, 'G', 3959-3974, 'A', 3976-3991, 'G', 3993-4008, 'A', 4010-4025, 'G', 4027-4042, 'A', 4044-4059, 'G', 4061-4076, 'A', 4078-4093, 'G', 4095-4110, 'A', 4112-4127, 'G', 4129-4144, 'A', 4146-4161, 'G', 4163-4178, 'A', 4180-4195, 'G', 4197-4212, 'A', 4214-4229, 'G', 4231-4246, 'A', 4248-4263, 'G', 4265-4280, 'A', 4282-4297, 'G', 4299-4314, 'A', 4316-4331, 'G', 4333-4348, 'A', 4350-4365, 'G', 4367-4382, 'A', 4384-4399, 'G', 4401-4416, 'A', 4418-4433, 'G', 4435-4450, 'A', 4452-4467, 'G', 4469-4484, 'A', 4486-4501, 'G', 4503-4518, 'A', 4520-4535, 'G', 4537-4552, 'A', 4554-4569, 'G', 4571-4586, 'A', 4588-4603, 'G', 4605-4620, 'A', 4622-4637, 'G', 4639-4654, 'A', 4656-4671, 'G', 4673-4688, 'A', 4690-4705, 'G', 4707-4722, 'A', 4724-4739, 'G', 4741-4756, 'A', 4758-4773, 'G', 4775-4790, 'A', 4792-4807, 'G', 4809-4824, 'A', 4826-4841, 'G', 4843-4858, 'A', 4860-4875, 'G', 4877-4892, 'A', 4894-4909, 'G', 4911-4926, 'A', 4928-4943, 'G', 4945-4960, 'A', 4962-4977, 'G', 4979-4994, 'A', 4996-5011, 'G', 5013-5028, 'A', 5030-5045, 'G', 5047-5062, 'A', 5064-5079, 'G', 5081-5096, 'A', 5098-5113, 'G', 5115-5130, 'A', 5132-5147, 'G', 5149-5164, 'A', 5166-5181, 'G', 5183-5198, 'A', 5200-5215, 'G', 5217-5232, 'A', 5234-5249, 'G', 5251-5266, 'A', 5268-5283, 'G', 5285-5300, 'A', 5302-5317, 'G', 5319-5334, 'A', 5336-5351, 'G', 5353-5368, 'A', 5370-5385, 'G', 5387-5402, 'A', 5404-5419, 'G', 5421-5436, 'A', 5438-5453, 'G', 5455-5470, 'A', 5472-5487, 'G', 5489-5504, 'A', 5506-5521, 'G', 5523-5538, 'A', 5540-5555, 'G', 5557-5572, 'A', 5574-5589, 'G', 5591-5606, 'A', 5608-5623, 'G', 5625-5640, 'A', 5642-5657, 'G', 5659-5674, 'A', 5676-5691, 'G', 5693-5708, 'A', 5710-5725, 'G', 5727-5742, 'A', 5744-5759, 'G', 5761-5776, 'A', 5778-5793, 'G', 5795-5810, 'A', 5812-5827, 'G', 5829-5844, 'A', 5846-5861, 'G', 5863-5878, 'A', 5880-5895, 'G', 5897-5912, 'A', 5914-5929, 'G', 5931-5946, 'A', 5948-5963, 'G', 5965-5980, 'A', 5982-5997, 'G', 5999-6014, 'A', 6016-6031, 'G', 6033-6048, 'A', 6050-6065, 'G', 6067-6082, 'A', 6084-6099, 'G', 6101-6116, 'A', 6118-6133, 'G', 6135-6150, 'A', 6152-6167, 'G', 6169-6184, 'A', 6186-6201, 'G', 6203-6218, 'A', 6220-6235, 'G', 6237-6252, 'A', 6254-6269, 'G', 6271-6286, 'A', 6288-6303, 'G', 6305-6320, 'A', 6322-6337, 'G', 6339-6354, 'A', 6356-6371, 'G', 6373-6388, 'A', 6390-6405, 'G', 6407-6422, 'A', 6424-6439, 'G', 6441-6456, 'A', 6458-6473, 'G', 6475-6490, 'A', 6492-6507, 'G', 6509-6524, 'A', 6526-6541, 'G', 6543-6558, 'A', 6560-6575, 'G', 6577-6592, 'A', 6594-6609, 'G', 6611-6626, 'A', 6628-6643, 'G', 6645-6660, 'A', 6662-6677, 'G', 6679-6694, 'A', 6696-6711, 'G', 6713-6728, 'A', 6730-6745, 'G', 6747-6762, 'A', 6764-6779, 'G', 6781-6796, 'A', 6798-6813, 'G', 6815-6830, 'A', 6832-6847, 'G', 6849-6864, 'A', 6866-6881, 'G', 6883-6898, 'A', 6900-6915, 'G', 6917-6932, 'A', 6934-6949, 'G', 6951-6966, 'A', 6968-6983, 'G', 6985-7000, 'A', 7002-7017, 'G', 7019-7034, 'A', 7036-7051, 'G', 7053-7068, 'A', 7070-7085, 'G', 7087-7102, 'A', 7104-7119, 'G', 7121-7136, 'A', 7138-7153, '

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Db      102 KSCRNPPDPVNGVAVHIKIGIOFGSOIKYSCITGRIILGSSSNTCLISDGTIVMDNETIC 161
Oy      122 DRPGCLPPTIANGDFTSISREYFHGSVYTYHCLUGSGKKVPELVBPSTYCTSKDDQ 181
Db      162 DRPGCLPPTIANGDFTSISREYFHGSVYTYHCLUGSGKKVPELVBPSTYCTSKDDQ 221
Oy      182 VGIWSGPAPQCIIIPNK 197
Db      222 VGIWSGPAPQCIIIPNK 237

RESULT      2
A:Accession: A34924
complement C3b/C4b receptor-like protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 27-Jul-1990 #sequence_revision 11-Apr-1997 #text_change 03-Dec-1999
C:Accession: A34922; S03292
R:Hourcade, D.; Mesner, D.R.; Bee, C.; Zeldes, W.; Atkinson, J.P.
J. Biol. Chem. 265, 974-980, 1990
A>Title: Duplication and divergence of the amino-terminal coding region of the comple
A:Reference number: A34924; MUID:90110163
A:Accession: A34924
A:Molecule type: DNA
A:Residues: 1-479 <HO2>
A:Cross-references: GB:J05195
R:Hourcade, D.; Mesner, D.R.; Atkinson, J.P.; Holers, V.M.
J. Exp. Med. 168, 1255-1270, 1988
A>Title: Identification of an alternative polyadenylation site in the human C3b/C4b r
type 1.
A:Reference number: S03291; MUID:89010527
A:Accession: S03292
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 7FFFAFR',452-482 <HO2>
A:Cross-references: EMBL:X14360
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, November 1988
F:43-99/Domain: complement factor H repeat homology <FH01>
F:104-161/Domain: complement factor H repeat homology <FH02>
F:166-232/Domain: complement factor H repeat homology <FH03>
F:238-293/Domain: complement factor H repeat homology <FH04>
F:297-353/Domain: complement factor H repeat homology <FH05>
F:358-416/Domain: complement factor H repeat homology <FH06>
F:421-478/Domain: complement factor H repeat homology <FH07>

Query Match      94.0%; Score 1038; DB 2; Length 482;
Best Local Similarity 93.9%; Pred. No. 1,5e-85;
Matches 184; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Oy      2  CCNAPEMLPFARPNLNLDEFEFPITGTYLNTBCRGYSGRPSITCLKNSWGTAKDRCR 61
Db      42  CCNPEWMLPFAFAPNLNLDEFEFPITGTYLNTBCRGYSGRPSITCLKNSWTSKDKCR 101
Oy      62  KSCRNPDPVNGVAVHIKIGIOFGSOIKYSCITGRIILGSSSNTCLISDGTIVMDNETIC 121
Db      102 KSCRNPDPVNGVAVHIKIDIOFRSQIKYSCKGRILGSSSNTCLISGNTVIMDKTPVC 161
Oy      122 DRPGCLPPTIANGDFTSISREYFHGSVYTYHCLUGSGKKVPELVBPSTYCTSKDDQ 181
Db      162 DRPGCLPPTIANGDFTSISREYFHGSVYTYHCLUGSGKKVPELVBPSTYCTSKDDQ 221
Oy      182 VGIWSGPAPQCIIIPNK 197
Db      222 VGIWSGPAPQCIIIPNK 237

RESULT      3
complement receptor 1 - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I36936; I36937

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R: Birmingham, D.J.; Shen, X.P.; Hourcade, D.; Nickells, M.W.; Atkinson, J.P.
 J. Immunol. 153, 691-700, 1994
 A:Title: Primary sequence of an alternatively spliced form of CRI. Candidate for the 75,
 A:Reference number: I36935; MUID:94292799
 A:Accession: I36936
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2014 <BIR1>
 A:Cross-references: GB:I24920; NID:9551564; PIDN:AA51438.1; PID:9557725
 A:Accession: I36937
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-397,1751-2014 <BIR2>
 A:Cross-references: GB:I24921; NID:9557726; PIDN:AA51439.1; PID:9557727
 A:Gene: CRI
 C:Superfamily: C4b-binding protein alpha chain; complement factor F repeat homology
 C:Keywords: duplication; glycoprotein; tandem repeat
 F:18-74/Domain: complement factor H repeat homology <FH01>
 F:79-136/Domain: complement factor H repeat homology <FH02>
 F:141-207/Domain: complement factor H repeat homology <FH03>
 F:213-268/Domain: complement factor H repeat homology <FH04>
 F:272-328/Domain: complement factor H repeat homology <FH05>
 F:333-391/Domain: complement factor H repeat homology <FH06>
 F:396-462/Domain: complement factor H repeat homology <FH07>
 F:470-526/Domain: complement factor H repeat homology <FH08>
 F:529-586/Domain: complement factor H repeat homology <FH09>
 F:722-778/Domain: complement factor H repeat homology <FH10>
 F:1041-1107/Domain: complement factor H repeat homology <FH11>
 F:1172-1228/Domain: complement factor H repeat homology <FH12>
 F:1233-1291/Domain: complement factor H repeat homology <FH13>
 F:1296-1362/Domain: complement factor H repeat homology <FH14>
 F:1432-1489/Domain: complement factor H repeat homology <FH15>
 F:1625-1681/Domain: complement factor H repeat homology <FH16>
 F:1749-1815/Domain: complement factor H repeat homology <FH17>
 F:1833-1879/Domain: complement factor H repeat homology <FH18>
 F:1884-1940/Domain: complement factor H repeat homology <FH19>

Query Match 93.2%; Score 1029; DB 2; Length 2014;
 Best Local Similarity 93.9%; Pred. No. 4,4e-84;
 Matches 184; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 QCNAPFWLPARPNTLDEFFPIGTYLNECRPGYSGRPFSTICLKNWYTGAKRCRR 61
 DB 17 QCNAPFWLPARPNTLDEFFPIGTYLNECRPGYSGRPFSTICLKNWYTGAKRCRR 76
 QY 62 KCRNPDPVNGMVAHYIKIGIOFSGQIKYCTKGYRLIGSSSACITISGDTVIMDNPTPIC 121
 DB 77 KCRNPDPVNGMVAHYIKIGIOFSGQIKYCTKGYRLIGSSSACITISGDTVIMDNPTPIC 136
 QY 122 DRIPGCLPTIANGDFTSISREYFHGVSYYTYHCNLSGRKKVFLVGEPSICTSKDDQ 181
 DB 137 DRIPGCLPTIANGDFTSISREYFHGVSYYTYHCNLSGRKKVFLVGEPSICTSKDDQ 196
 QY 182 VGIWSPAPQCIIPNK 197
 DB 197 VGIWSPAPQCIIPNK 212

RESULT 4
 A43519
 Complement receptor CRI precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Oct-1992 #sequence_revision 30-Jan-1993 #text_change 19-May-2000
 C:Accession: A43519
 J:Paul, M.S.; Aegeerter, M.; Cepak, K.; Miller, M.D.; Wells, J.H.
 J. Immunol. 144, 1988-1996, 1990
 A:Title: The murine complement receptor gene family. The genomic and transcriptional com
 A:Reference number: A43519; MUID:90171600
 A:Accession: A43519
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-440 <PAU>
 A:Cross-references: GB:M34164
 A:Note: The authors translated the codon GGC for residue 21 as Ala, and CAG for resid
 C:Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
 F:42-98/Domain: complement factor H repeat homology <FH1>
 F:103-160/Domain: complement factor H repeat homology <FH2>
 F:165-231/Domain: complement factor H repeat homology <FH3>
 F:237-293/Domain: complement factor H repeat homology <FH4>
 F:299-355/Domain: complement factor H repeat homology <FH5>

Query Match 63.6%; Score 702; DB 2; Length 440;
 Best Local Similarity 63.1%; Pred. No. 1.8e-55;
 Matches 124; Conservative 22; Mismatches 49; Indels 0; Gaps 0;

QY 3 CNAPEWLPARPNTLDEFFPIGTYLNECRPGYSGRPFSTICLKNWYTGAKRCRR 62
 DB 42 CPAPQLPSAKPNTLDESMFPIGTYLNECRPGYSGRPFSTICLKNWYTGAKRCRR 101
 QY 63 SCRNPPDPVNGMVAHYIKIGIOFSGQIKYCTKGYRLIGSSSACITISGDTVIMDNPTPIC 122
 DB 102 QCKTPSDPENGLVHATGIEFGSRINVTGNOGYRLIGSSSACITISGDTVIMDNPTPIC 161
 QY 123 RIPCGLPTIANGDFTSISREYFHGVSYYTYHCNLSGRKKVFLVGEPSICTSKDDQ 182
 DB 162 WIPCELPPIPGIDFSSSTREDFHGMVYTYRCNDARAKALFNLVGEPSICTSKDDQ 221
 QY 183 GIWSPAPQCIIPNK 197
 DB 222 GIWSPAPQCIIPNK 236

RESULT 5
 A30550
 Complement C3b/C4b receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 19-May-2000
 C:Accession: A30550
 J:Paul, M.S.; Aegeerter, M.; O'Brien, S.E.; Kurtz, C.B.; Wells, J.H.
 J. Immunol. 142, 582-589, 1989
 A:Title: The murine complement receptor gene family. Analysis of mCRY gene products a
 A:Reference number: A30550; MUID:89093944
 A:Accession: A30550
 A:Status: preliminary
 A:Molecule type: mRNA
 C:Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
 F:103-160/Domain: complement factor H repeat homology <FH2>
 F:165-231/Domain: complement factor H repeat homology <FH3>
 F:237-293/Domain: complement factor H repeat homology <FH4>
 F:299-355/Domain: complement factor H repeat homology <FH5>

Query Match 63.3%; Score 699; DB 2; Length 433;
 Best Local Similarity 63.1%; Pred. No. 3.2e-55;
 Matches 123; Conservative 23; Mismatches 49; Indels 0; Gaps 0;

QY 3 CNAPEWLPARPNTLDEFFPIGTYLNECRPGYSGRPFSTICLKNWYTGAKRCRR 62
 DB 42 CPAPQLPSAKPNTLDESMFPIGTYLNECRPGYSGRPFSTICLKNWYTGAKRCRR 101
 QY 63 SCRNPPDPVNGMVAHYIKIGIOFSGQIKYCTKGYRLIGSSSACITISGDTVIMDNPTPIC 122
 DB 102 QCKTPSDPENGLVHATGIEFGSRINVTGNOGYRLIGSSSACITISGDTVIMDNPTPIC 161
 QY 123 RIPCGLPTIANGDFTSISREYFHGVSYYTYHCNLSGRKKVFLVGEPSICTSKDDQ 182
 DB 162 WIPCELPPIPGIDFSSSTREDFHGMVYTYRCNDARAKALFNLVGEPSICTSKDDQ 221
 QY 183 GIWSPAPQCIIPNK 197
 DB 222 GIWSPAPQCIIPNK 236

QY	129	PTTANGDFTSISREYF	145
Db	314	PGGINDGFSTSTREDF	330
QY	9	B26359	
decay-accelerating factor, GPI-anchored splice form precursor - human			
N:Alternate names:	CD55; DAF splice form 2; decay-accelerating factor membrane-bound form		
C:Species:	Homo sapiens (man)		
C:Date:	05-Oct-1988	#sequence, revision 16-Aug-1996 #text, change 02-Jun-2000	
C:Accession:	B26359; A27666; A39101; I52594; I52564		
R:Caras, I.W.; Davitt, M.A.; Rhee, L.; Meddell, G.; Martin Jr., D.W.; Nussenzweig, V.			
Nature 325, 545-549, 1987			
A:Title:	Cloning of decay-accelerating factor suggests novel use of splicing to generate		
A:Reference number:	A26359; MUID:87115845		
A:Accession:	B26359		
A:Molecule type:	mRNA		
A:Residues:	1-381 <CAR>		
A:Cross-references:	GB:572858; NID:g181464; PIDN:AAA52168.1; PID:g181465		
R:Medof, M.E.; Lublin, D.M.; Holes, V.M.; Ayers, D.J.; Gelly, R.R.; Leykam, J.F.; Atkinson			
Proc. Natl. Acad. Sci. U.S.A. 84, 2007-2011, 1987			
A:Title:	Cloning and characterization of cDNAs encoding the complete sequence of decay-ac		
A:Reference number:	A27666; MUID:87115602		
A:Accession:	A27666		
A:Molecule type:	mRNA		
A:Residues:	6-79, 'T', 81-84, 'M', 86-381 <MED>		
A:Cross-references:	GB:M5799; NID:g181462; PIDN:AAA52167.1; PID:g181463		
R:Moran, P.; Raab, H.; Kohr, W.J.; Caras, I.W.			
J. Biol. Chem. 266, 1250-1257, 1991			
A:Title:	Glycophospholipid membrane anchor attachment. Molecular analysis of the cleavag		
A:Reference number:	A39101; MUID:91093238		
A:Accession:	A39101		
A:Molecule type:	protein		
A:Residues:	338-352 <MOR>		
R:Lublin, D.M.; Mallinson, G.; Poole, J.; Reid, M.E.; Thompson, E.S.; Ferdman, B.R.; Tel			
Blood 84, 1276-1282, 1994			
A:Title:	Molecular basis of reduced or absent expression of decay-accelerating factor in		
A:Reference number:	I52594; MUID:94325573		
A:Accession:	I52594		
A>Status:	translated from GB/EMBL/DBJ		
A:Molecule type:	DNA		
A:Residues:	194-198, 'L', 200-209 <LUB>		
A:Cross-references:	GB:572858; NID:g639599; PIDN:AAAC6063.1; PID:g639600		
A:Experimental source:	Individual KW, Cromer blood group phenotype Dr(a-)		
A>Note:	the single nucleotide difference in this allele, which changes Ser-199 to Leu, 1		
on (see reference I52564), and thus reduced DAF expression			
R:Reid, M.E.; Mallinson, G.; SIm, R.B.; Poole, J.; Pausch, V.; Merry, A.H.; Liew, Y.W.;			
Blood 79, 3291-3297, 1991			
A:Title:	Biochemical studies on red blood cells from a patient with the Inab phenotype (
A:Reference number:	I52564; MUID:92075980		
A:Accession:	I52564		
A>Status:	translated from GB/EMBL/DBJ		
A:Molecule type:	mRNA		
A:Residues:	190-193, 'OLCPVF', <RE2>		
A:Cross-references:	GB:570688; NID:g240301; PIDN:AAAB20576.1; PID:g240302		
A:Experimental source:	Individual KW, Cromer blood group phenotype Dr(a-)		
C:Comment:	Cromer blood group system antigens reside on this protein.		
C:Comment:	For an alternative splice form, see PIR:A26359		
C:Genetics:			
A:Gene:	GDB:DAF		
A:Cross-references:	GDB:119088; OMTM:125240		
C:Map position:	Iq32-Iq32		
C:Function:			
A:Description:	protects tissues from damage by regulating complement activation on cell		
A:Superfamily:	decay-accelerating factor; complement factor H repeat homology		
C:Keywords:	alternative splicing; blocked carboxyl end; complement inhibitor; glycoprotein		
F:1-34/Domain:	signal sequence #status predicted <SIG>		
F:35-353/Product:	decay-accelerating factor 2 #status predicted <MAT>		

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F:98-158/Domain: complement factor H repeat homology <FH02>
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F:225-283/Domain: complement factor H repeat homology <FH04>
F:354-381/Domain: carboxyl-terminal propeptide #status predicted <PRO>
F:95/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:355/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature f
Query Match          37.0%   Score 408; DB 1; Length 381;
Best Local Similarity 42.6%; Pred. No. 3,5e-29;
Matches    83; Conservative    29; Mismatches    69; Indels    14; Gaps    6;

QY      3 CNAPEMLPFA--RPTNLDEFEFFIGTYLNYECRRGYSGRPF---SIICKNSWYGAKD 57
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DB     98 CEVFRILNLSASLKQIYITQNT-FPGVTVEYECRGYRREPSLSPKLIQLCNLRSTAVE 156
QY      58 RCRRSKSCNPDPNVGNMVAHYIKGIQFGSQIKYISCTKGTRILIGSSSATICISGDVIYDNE 117
           | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     157 FCKRKSCNPBEIRNGQIDVPGGLIFGATISFCSTYGTKELGSTSFLLIGSSSVOWSDP 216
QY      118 TPICRIPCGGAPPTIANDPFTSIREYHVSYSVTHYCNLGSRRKKVELVGESIVCTS 177
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     217 LPECETICTAPPPOIDNKIIQG-EKHDTGYQSOTYACNKG-----FTMGEHSITCTV 269
QY      178 KDDQVINGSGAPQC 192
           | : | | | | | | | |
DB     270 NNDE-GEMSGPPPEC 283
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RESULT    10
A26359
decay-accelerating factor, splice form 1 precursor - human
N.Alternate names: decay-accelerating factor 5; decay-accelerating factor secreted for
C.Species: Homo sapiens (man)
C.Date: 05-Oct-1988 #sequence-revision 05-Oct-1988 #text-change 02-Jun-2000
C.Accession: A26359; A39702; S16187; S23138; A27258
R.Catanz, I.W.; Davilts, M.A.; Rhee, L.; Meddell, G.; Martin Jr., D.W.; Nussenzweig, V.
Nature 325, 545-549, 1987
A.Title: Cloning of decay-accelerating factor suggests novel use of splicing to gener
A.Reference number: A26359; MUID:87115845
A.Accession: A26359
A.Molecule type: mRNA
A.Residues: 1-440 <CAR>
A.Cross-references: GB:M30142
R.Emlonu, U.K.; Ravl, L.; Medof, M.E
Proc. Natl. Acad. Sci. U.S.A. 88, 4675-4679, 1991
A.Title: Characterization of the decay-accelerating factor gene promoter region.
A.Reference number: A39702; MUID:91271256
A.Accession: A39702
A.Molecule type: DNA
A.Residues: 1-79, 'T', 81-104 <END>
A.Cross-references: GB:M64356
A.Note: The authors translated the codon AGT for residue 85 as Met
R.Nakano, Y.; Sugita, Y.; Ishikawa, Y.; Choi, N.H.; Tobe, T.; Tomita, M.
Biochim. Biophys. Acta 1074, 326-330, 1991
A.Title: Isolation of two forms of decay-accelerating factor (DAF) from human urine.
A.Reference number: S16187; MUID:91291869
A.Accession: S16187
A.Status: preliminary
A.Molecule type: protein
A.Residues: 35-47 <BIO>
R.Nakano, Y.; Sumida, K.; Kikuta, N.; Miura, N.H.; Tobe, T.; Tomita, M.
Biochim. Biophys. Acta 1116, 235-240, 1992
A>Title: Complete determination of disulfide bonds localized within the short consensu
A.Reference number: S23138; MUID:92305034
A.Accession: S23138
A.Status: preliminary
A.Molecule type: protein
A.Residues: 35-41,65-68;79-81;93-103;128-134;143-145;155-159;162-168;188-192;203-204;
R.Sugita, Y.; Negro, T.; Matsuda, T.; Sakamoto, T.; Tomita, M.
J. Biochem. 100, 143-150, 1986
A>Title: Improved method for the isolation and preliminary characterization of human

```

A:Reference number: A27258; MUID:87008461
 A:Accession: A27258
 A:Molecule type: protein
 A:Residues: 35 'X', 37 'G', 39-51 'P', 53-55 'X', 57-58 'X', 60-63 <Stu>
 A:Note: Gly-35 and Leu-38 were also found
 C:Comment: For an alternative splice form, see PIR:B26359
 C:Gene: GDB:DAF
 A:Cross-references: GDB:119088; OMIM:125240
 A:Map position: 1q32-1q32
 C:Superfamily: decay-accelerating factor; complement factor H repeat homology
 C:Keywords: alternative splicing; glycoprotein
 F:1-34/Domain: signal sequence #status predicted <Sig>
 F:35-44/Domain: decay-accelerating factor 1 #status predicted <Mat>
 F:36-94/Domain: complement factor H repeat homology <FH01>
 F:98-158/Domain: complement factor H repeat homology <FH02>
 F:163-220/Domain: complement factor H repeat homology <FH03>
 F:225-283/Domain: complement factor H repeat homology <FH04>
 F:95/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.0%; Score 408; DB 2; Length 440;
 Best Local Similarity 42.6%; Pred. No. 4.1e-29;
 Matches 83; Conservative 29; Mismatches 69; Indels 14; Gaps 6;

3 CNAPEWLPFA--RPTNLDEFEPIGTLYNCEKRGYSGRPF---SITLKNVMTGAKD 57
 98 CEVPRFLNLSAKLPYITONY-FPVSTVVEYECRPEYRREPSISPKLTGLNKNSTAVE 156
 58 RRRKRSRNPDPVNGVAVHYIKIGIOGSOIKYSGTKGYRLIGSSATCIISGDTVIMDNE 117
 157 FCKKRSRNPDPVNGVAVHYIKIGIOGSOIKYSGTKGYRLIGSSATCIISGSSVQMSDP 216
 118 TPICRIPGCLPPTIANGDFTSISREYFHYSVYTHCNLSRGKVFELVGEPSIYCT 177
 217 LPECEITCPAPQIDNGIIOG-ERDHYGYSQSVTYACNKG-----FTMGEHSIYCTV 269
 178 KDQVGIWSGPAPQC 192
 270 NMDE-GEWSGPPEPC 283

RESULT 11
 156234
 decay-accelerating factor - orangutan (fragment)
 C:Species: Pongo pygmaeus (orangutan)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
 C:Accession: 156234
 R:Nickells, M.R.; Alvarez, J.I.; Lublin, D.M.; Atkinson, J.P.
 J. Immunol. 152, 676-685, 1994
 A:Title: Characterization of DAF-2, a high molecular weight form of decay-accelerating factor
 A:Reference number: 156234; MUID:94110622
 A:Accession: 156234
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-340 <RES>
 A:Cross-references: GB:S67775; NID:9459389; PIDN:AAC60609.1; PID:9459390
 C:Superfamily: decay-accelerating factor; complement factor H repeat homology
 F:1-53/Domain: complement factor H repeat homology (fragment) <FH01>
 F:57-117/Domain: complement factor H repeat homology <FH02>
 F:122-179/Domain: complement factor H repeat homology <FH03>
 F:184-242/Domain: complement factor H repeat homology <FH04>

Query Match 36.6%; Score 404; DB 2; Length 340;
 Best Local Similarity 41.8%; Pred. No. 7.1e-29;
 Matches 82; Conservative 30; Mismatches 68; Indels 16; Gaps 7;

3 CNAPEWLPFA--RPTNLDEFEPIGTLYNCEKRGYSGRPF---SITLKNVMTGAK 56
 57 CEVPRFLNLSAKLPYITONY-FPVSTVVEYECRPEYRREPSISPKLTGLNKNSTAVE 114
 57 DRCRRKRSRNPDPVNGVAVHYIKIGIOGSOIKYSGTKGYRLIGSSATCIISGDTVIMDN 116

DB 115 EFCKKRSRNPDPVNGVAVHYIKIGIOGSOIKYSGTKGYRLIGSSATCIISGSSVQMSD 174
 117 EPICDRICGCLPPTIANGDFTSISREYFHYSVYTHCNLSRGKVFELVGEPSIYCT 176
 175 PLPECEITCPAPQIDNGIIOG-KRDHYGYSQSVTYACNKG-----FTMGEHSIYCT 227
 177 SKDQVGIWSGPAPQC 192
 228 VMDDE-GEWSGPPEPC 242

RESULT 12
 557953
 C4b protein alpha chain precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
 C:Accession: S57953
 R:Hiillarp, A.; Thern, A.; Dahlback, B.
 Submitted to the EMBL Data Library, July 1995
 A:Description: Molecular cloning of rat C4b-binding protein alpha- and beta-chains: s
 A:Reference number: S57953
 A:Accession: S57953
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-958 <Hili>
 A:Cross-references: EMBL:Z50051; NID:9899379; PIDN:CAA90391.1; PID:9899380
 C:Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
 F:15-72/Domain: complement factor H repeat homology <FH1>
 F:77-134/Domain: complement factor H repeat homology <FH2>
 F:139-199/Domain: complement factor H repeat homology <FH3>
 F:204-258/Domain: complement factor H repeat homology <FH4>
 F:263-324/Domain: complement factor H repeat homology <FH5>
 F:328-386/Domain: complement factor H repeat homology <FH6>
 F:390-443/Domain: complement factor H repeat homology <FH7>
 F:447-501/Domain: complement factor H repeat homology <FH8>

Query Match 33.6%; Score 370.5; DB 2; Length 558;
 Best Local Similarity 41.5%; Pred. No. 1.2e-25;
 Matches 80; Conservative 22; Mismatches 82; Indels 9; Gaps 3;

2 CNAPEWLPFA--RPTNLDEFEPIGTLYNCEKRGYS--GRPSITLKNVMTGAKDRC 59
 14 KCGPPDLPLALPSAKMKTDFESHTRYNCRGYSASSQSILYKPLCKWQ-INIAC 72
 60 RRRKRSRNPDPVNGVAVHYIKIGIOGSOIKYSGTKGYRLIGSSATCIISGDTVIMDNETP 119
 73 VKKRSRNPDPVNGVAVHYIKIGIOGSOIKYSGTKGYRLIGSSATCIISGDTVIMDNETP 132
 120 ICDRIPLGCLPPTIANGDFTSISREYFHYSVYTHCNLSRGKVFELVGEPSIYCTSKD 179
 133 ECVIACGMPDINSNGKHNGREEFYRSSVYTKD-----PDFLLGNASTITCYVN 186
 180 DQVGIWSGPAPQC 192
 187 KTVGVMSPPPTC 199

RESULT 13
 A46458
 human CRI homology CRP - guinea pig
 C:Species: Cavita porcellus (guinea pig)
 C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 07-Jul-1995
 C:Accession: A46458
 R:Moore Jr., F.D.
 J. Immunol. 147, 3615-3622, 1991
 A:Title: CRP: a guinea pig protein, identified by sequence homology to human CRI, wh
 A:Reference number: A46458; MUID:92043737
 A:Accession: A46458
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-211 <MOO>

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2001, 13:41:15 ; Search time 32.86 Seconds

(without alignments)
193.607 Million cell updates/sec

Title: US-09-380-682-1

Perfect score: 1104
Sequence: 1 MGNAPFWLFFARPTNLTDE.....KDOGVGIMSGPAPQCIIIPNK 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues
Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1042	94.4	2039 1	CRI_HUMAN
2	437.5	39.6	390 1	DAF1_MOUSE
3	413.5	37.5	407 1	DAF2_MOUSE
4	408	37.0	381 1	DAF_HUMAN
5	404	36.6	340 1	DAF_PONPY
6	370.5	33.6	558 1	C4BP_RAT
7	364.5	33.0	507 1	DAF_CAVPO
8	364.5	33.0	610 1	CR2_BOVIN
9	335.5	30.4	1025 1	C4BP_MOUSE
10	325.5	29.5	469 1	C4BP_MOUSE
11	315.5	28.6	597 1	C4BP_HUMAN
12	295	26.7	377 1	MCP_HUMAN
13	292	26.4	360 1	CCPH_HSVSA
14	290.5	26.3	1033 1	CR2_HUMAN
15	288.5	25.1	263 1	VCP_VACCV
16	251	22.7	1234 1	CFRH_MOUSE
17	234.5	21.2	1231 1	CFRH_HUMAN
18	212	19.2	768 1	LEM3_MOUSE
19	212	19.2	768 1	LEM3_RAT
20	200.5	18.2	769 1	LEM3_SHEEP
21	188.5	17.1	830 1	LEM3_HUMAN
22	187.5	17.0	484 1	LEM2_PIG
23	187.5	17.0	668 1	F13B_MOUSE
24	187	16.9	611 1	LEM2_CANFA
25	186	16.8	646 1	LEM3_BOVIN
26	183	16.6	610 1	LEM2_HUMAN
27	182.5	16.5	551 1	LEM2_RABIT
28	176.5	16.0	331 1	CFHD_HUMAN
29	176	15.9	258 1	C4BB_HUMAN
30	176	15.9	958 1	H1G_PROME
31	173	15.7	1019 1	LFC_CARO
32	172.5	15.6	330 1	CFH1_HUMAN
33	172	15.6	345 1	APOH_CANFA

ALIGNMENTS

```

RESULT 1
ID CRI_HUMAN
AC P17927:
DR 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3b/C4b RECEPTOR) (CD35
DE ANTIGEN).
GN CRI OR C3bR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8903592; PubMed=2972794;
RA Klickstein L.B., Barlow T.J., Miletic V., Rabson L.D., Smith J.A.,
RA Fearon D.T.;
RT "Identification of distinct C3b and C4b recognition sites in the
RT human C3b/C4b receptor (CRI, CD35) by deletion mutagenesis.";
RL J. Exp. Med. 168:1699-1717(1988).
RN [2]
RP SEQUENCE OF 503-2039 FROM N.A.
RX MEDLINE=87168191; PubMed=2951479;
RA Klickstein L.B., Wong W.W., Smith J.A., Wels J.H., Wilson J.G.,
RA Fearon D.T.;
RT "Human C3b/C4b receptor (CRI). Demonstration of long homologous
RT repeating domains that are composed of the short consensus repeats
RT characteristics of C3/C4 binding proteins.";
RL J. Exp. Med. 165:1095-1112(1987).
RN [3]
RP SEQUENCE OF 761-783; 831-845 AND 1179-1195 FROM N.A.
RX MEDLINE=86067975; PubMed=2933745;
RA Wong W.W., Klickstein L.B., Smith J.A., Wels J.H., Fearon D.T.;
RT "Identification of a partial cDNA clone for the human receptor for
RT complement fragments C3b/C4b.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7711-7715(1985).
CC -I- FUNCTION: CRI, PRESENT ON ERYTHROCYTES, LEUCOCYTES, GLOMERULAR
CC PODOCYTES, AND SPLENIC FOLLICULAR DENDRITIC CELLS, MEDIATES THE
CC BINDING BY THESE CELLS OF PARTICLES AND IMMUNE COMPLEXES THAT HAVE
CC ACTIVATED COMPLEMENT.
CC -I- SUBUNIT: MONOMER.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- POLYMORPHISM: CRI IS RESPONSIBLE FOR THE KNOX BLOOD GROUP SYSTEM.
CC -I- MISCELLANEOUS: SEVEN SHORT CONSENSUS REPEATS (SCR) CONSTITUTE A
CC LONG HOMOLOGOUS REPEAT (LHR). THE N-TERMINAL TWO SRCS OF LHR-A
CC CONTAINED A SITE DETERMINING C4 SPECIFICITY, AND THE N-TERMINAL
CC TWO SRCS OF LHR-B AND -C EACH HAD A SITE DETERMINING C3
CC SPECIFICITY.
CC -I- MISCELLANEOUS: THIS IS THE SEQUENCE OF THE F ALLOTYPE OF CRI.
CC -I- SIMILARITY: CONTAINS 30 SUSHI (SCR) REPEATS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Query Match 94.4%; Score 1042; DB 1; Length 2039;
 Best Local Similarity 94.9%; Pred. No. 1,1e-87;
 Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNPENLPAPRPNLTDEFEPIGTYLNECRPGYSGRPSITCLKNSVTGAKDCRCR 61
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 DB 42 QCNPENLPAPRPNLTDEFEPIGTYLNECRPGYSGRPSITCLKNSVTGAKDCRCR 101
 |||||

QY 62 KSCRNPPDPVNGMVHVITKIQFGSQIKYSCGRYRLIGSSATCIISGDTYIMDNPTPIC 121
 |||||
 DB 102 KSCRNPPDPVNGMVHVITKIQFGSQIKYSCGRYRLIGSSATCIISGDTYIMDNPTPIC 161
 |||||

QY 122 DRIPCGLPPTIANGDFTSISREHYGVSVTYHCNLSRGKRVLYGEPSTYCTSDQ 181
 |||||
 DB 162 DRIPCGLPPTIANGDFTSISREHYGVSVTYHCNLSRGKRVLYGEPSTYCTSDQ 221
 |||||

QY 182 VGIMSGPAPCIIIPNK 197
 |||||
 DB 222 VGIMSGPAPCIIIPNK 237
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RESULT 2
 ID DAF1_MOUSE STANDARD; PRT; 390 AA.
 AC 061475; 061397; p97732;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE COMPLEMENT DECAY-ACCELERATING FACTOR, GPI-ANCHORED PRECURSOR
 DE (DAF-GPI).
 GN DAF1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-G57B/6J; TISSUE-TESTIS;
 RA MEDLINE=95403982; PubMed=7545711;
 RA Spicer A.P., Seidlin M.F., Gendler S.J.;
 RT "Molecular cloning and chromosomal localization of the mouse decay-
 accelerating factor genes. Duplicated genes encode
 RT glycosylphosphatidylinositol-anchored and transmembrane forms.";
 RT J. Immunol. 153:3079-3091(1995).
 RL [2]
 RN SEQUENCE OF 7-390 FROM N.A.
 RP STRAIN-BALB/C; TISSUE-SPLEEN;
 RC MEDLINE=96362213; PubMed=8671624;
 RA Fukunaka Y., Yasui A., Okada N., Okada H.;
 RT "Molecular cloning of murine decay accelerating factor by
 RT immunoscreening.";
 RT Int. Immunol. 8:379-385(1996).
 RL [1]
 CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- TISSUE SPECIFICITY: BRAIN, SECRETORY EPITHELIA, SKELETAL MUSCLE,
 CC LIVER, TESTES, THYMUS, SPLEEN AND LYMPH NODE.
 CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
 CC FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE
 CC ACTIVE SITE ON SCR3 (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
 CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
 CC (RCA) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L41366; AAB00091.1; -

DR EMBL: D63679; BAA09830.1; -
 DR .HSSP: P08603; 1HCC.
 DR WGD; MG1:104850; DAF1.
 DR INTERPRO: IPR000436; -
 DR PIRAM; PF00084; sush1; 4.
 KW Complement pathway; Glycoprotein; Membrane; Repeat; GPI-anchor;
 KM Signal; Sush1.
 FT SIGNAL 1 34
 FT CHAIN 35 361
 FT
 FT PROPER 362 390
 FT DOMAIN 35 285
 FT REPEAT 35 95
 FT REPEAT 97 159
 FT REPEAT 162 221
 FT REPEAT 224 285
 FT DOMAIN 288 364
 FT DISULFID 65 94
 FT DISULFID 98 145
 FT DISULFID 129 158
 FT DISULFID 163 204
 FT DISULFID 190 220
 FT DISULFID 225 267
 FT DISULFID 253 284
 FT CARBOHYD 187 187
 FT CARBOHYD 262 262
 FT LIPID 361 361
 FT CONFLICT 7 7
 FT CONFLICT 9 9
 FT CONFLICT 83 83
 FT CONFLICT 91 91
 FT CONFLICT 135 135
 FT CONFLICT 173 173
 FT CONFLICT 180 180
 FT SEQUENCE 390 AA; 42618 MW; 4418722DFF47F9E7 CRC64;

Query Match 39.6%; Score 437.5; DB 1; Length 390;
 Best Local Similarity 44.7%; Pred. No. 5.2e-33;
 Matches 92; Conservative 25; Mismatches 68; Indels 21; Gaps 6;

QY 3 QCNPENLPAPRPNLTDEFEPIGTYLNECRPGYSGR---PSITCLKNSVTGA 55
 |||||
 DB 98 CVAPERLSFA--SLKEYINMNEFPVGTIVEYECRGEFGEQPLPKATCLEDLVSPV 154
 |||||

QY 56 KDCRRKSCRNPPDPVNGMVHVITKIQFGSQIKYSCGRYRLIGSSATCIISGDTYIMD 115
 |||||
 DB 155 AQCFKRSKSCRNPPDLNGHINIPGILFGESEINFSCNPGIRLVGSSTFCVSTGNTVDM 214
 |||||

QY 116 NETPICDRIPCGLPPTIANGDFTSISREHYGVSVTYHCNLSRGKRVLYGEPSTYCT 175
 |||||
 DB 215 DEFVCTEICHPEPCKINNGIMRGEOSY--TYSQVVTYSCDKG-----FLVGNASTYC 267
 |||||

QY 176 TSKDDVGIMSGPAPCIIIPNK 197
 |||||
 DB 268 TVSKSDVGIMSGPAPCIIIPNK 293
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RESULT 3
 ID DAF2_MOUSE STANDARD; PRT; 407 AA.
 AC 061476;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE COMPLEMENT DECAY-ACCELERATING FACTOR, TRANSMEMBRANE PRECURSOR
 DE (DAF-TM).
 GN DAF2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.

RT "Characterization of DAF-2, a high molecular weight form of decay-
 RT accelerating factor (DAF; CD55), as a covalently cross-linked dimer
 of DAF-1."?
 RL J. Immunol. 152:676-685(1994).
 CC -1- FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT
 CC CONDENSE WITH CELL-SURFACE HYDROXYL OR AMINO GROUPS WHEN NASCENT
 CC C4B AND C3B ARE LOCALLY GENERATED DURING C4 AND C3 ACTIVATION.
 CC INTERACTION OF DAF WITH CELL-ASSOCIATED C4B AND C3B POLYPEPTIDES
 CC INTERFERES WITH THEIR ABILITY TO CATALYZE THE CONVERSION OF C2 AND
 CC FACTOR B TO ENZYMATICALLY ACTIVE C2A AND BB AND THEREBY PREVENTS
 CC THE FORMATION OF C4B2A AND C3BB, THE AMPLIFICATION CONVERTASES OF
 CC THE COMPLEMENT CASCADE (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENT
 CC HOMODIMER (MINOR FORM).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF DAF (DAF-2, SHOWN HERE, AND
 CC DAF-1) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
 CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
 CC FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE
 CC ACTIVE SITE ON SCR3 (BY SIMILARITY).
 CC -1- PM: THE SER/THR-RICH DOMAIN IS HEAVILY O-GLYCOSYLATED.
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
 CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
 CC (RCA) FAMILY.
 CC -----
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 CC -----
 CC EMBL: S67775; AAC60609.1; -.
 CC DR HSSP: P08603; IHFI.
 CC DR INTERPRO: IPR000436; -.
 CC DR PFM: PFO0084; sushl; 4.
 CC KW Complement pathway; Plasma; Glycoprotein; Membrane; Repeat;
 CC Alternative splicing; GPI-anchor; Sushl.
 CC FT NON_TER 1
 CC FT CHAIN 1 312
 CC FT PROPEP 313 340
 CC FT DOMAIN <1 243
 CC FT REPEAT 54
 CC FT REPEAT 56 118
 CC FT REPEAT 121 180
 CC FT REPEAT 183 243
 CC FT DOMAIN 246 315
 CC FT DISULFD 24 53
 CC FT DISULFD 57 104
 CC FT DISULFD 88 117
 CC FT DISULFD 122 163
 CC FT DISULFD 149 179
 CC FT DISULFD 184 226
 CC FT DISULFD 212 242
 CC FT CARBOHD 54 54
 CC FT CARBOHD 107 107
 CC FT LIFID 312 312
 CC FT SEQUENCE 340 AA; 37180 MW; D3D865C058204290 CRC64;
 Query Match 36.6%; Score 404; DB 1; Length 340;
 Best Local Similarity 41.8%; Pred. No. 5.3e-30;
 Matches 82; Conservative 30; Mismatches 68; Indels 16; Gaps 7;
 QY 3 CNAPEMLPFA--RPTNLDFEPEFGTYLVNCECRPGYSGRPS---ITCLNSWVTGAK 56
 DB 57 CEVPTRLNFAASKOPYITONT-FPVGTVEYVCRPEYR-RELSLSTKLCIDQNLWSTAV 114
 QY 57 DCRKRSKSNPPDPVGNVAVIKIGFSGQIRKSCYKRLIGSSATCIIISGDIYIMDN 116
 DB 115 EFCKKSKSCNPGEIRNGQIDVNSGLIFGATISFSCWTGYKLGPIPSLCLIGSSVQMSD 174

QY 117 EPIIDRIPCGPIPIANGDTISREFFHGSVYTYCNLSKRRKVFELVGEPSYCT 176
 DB 175 PLPECRREIYCAPQIDINGIIQG-KRDHYGYRSITYACNKG-----YTMGHSIYCT 227
 QY 177 SKDDGVIGSGPAPOC 192
 DB 228 VANDDE-GEMSGPDPPEC 242
 RESULT 6
 C4BP_RAT
 ID C4BP_RAT STANDARD; PRT; 558 AA.
 AC 063514;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR.
 GN C4BPA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
 RX MEDLINE-97166082; PubMed-9013975;
 RA Hillarp A., Wiklund H., Thern A., Dahlback B.;
 RT "Molecular cloning of rat C4b binding protein alpha- and beta-chains:
 RT structural and functional relationships among human, bovine, rabbit,
 RT mouse, and rat proteins.";
 RL J. Immunol. 158:1315-1323(1997).
 CC -1- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT
 CC ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR
 CC (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT
 CC ALSO ACCELERATES THE DEGRADATION OF THE C4B2A COMPLEX (C3
 CC CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA
 CC CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S
 CC AND WITH SERUM AMYLOID P COMPONENT.
 CC -1- SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS.
 CC -1- SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
 CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
 CC -----
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 CC EMBL: Z50051; CAA90391.1; -.
 CC DR HSSP: P10998; IYVC.
 CC DR INTERPRO: IPR000436; -.
 CC DR PFM: PFO0084; sushl; 8.
 CC KW Complement pathway; Plasma; Glycoprotein; Repeat; Sushl; signal.
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 CC FT CHAIN 1 558
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FT DISULFID 263 312 BY SIMILARITY.
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FT DISULFID 474 501 BY SIMILARITY.
FT DISULFID 509 509 INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
FT DISULFID 521 521 INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 491 491 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 558 AA: 62266 MW: 592FC0667ED15EFF CRC64;

Query Match 33.6%; Score 370.5; DB 1; Length 558;
Best Local Similarity 41.5%; Pred. No. 1.1e-26;
Matches 80; Conservative 22; Mismatches 82; Indels 9; Gaps 3;

OY 2 OCNAPMLPAPPTNLTFDEEPICTYLVNCRPGYS--GRPSIICLNKSVWTGAKDRG 59
DB 14 KCGPPDLRYALPASEMNTDPSHTTLKXNCRPGYSRASSOSLCKPLGKQ--INTAC 72
OY 60 RRKSCNPPDPVNGVNVKIGIOFSQIKYSCRGYRLIGSSSANTCIISGDTYIMNENP 119
DB 73 VKSCNPPDGLNGKVEKTDLFQSEIIEFSGEYILIGSSSTYCEIOGKGVSMEDPLP 132
OY 120 ICDRIPCGLPTIANGDFISREYHGVSVTYHGNLGRKGVYELVGEPSIYCTSD 179
DB 133 ECVIAKCGMPDISNKGHNGREEFYRASSVYKCD-----PDFTLLGNASITCTYVN 186
OY 180 DQVIGWSGPAPOC 192
DB 187 KTVGVWSPPSPPTC 199

RESULT 7
DAF_CAVPO STANDARD: PRT: 507 AA.
ID O60401; Q60402; Q60403; Q60404; Q60405; Q60406; P97254; P97255;
AC P97256;
DF 01-NOV-1997 (Rel. 35, Created)
DF 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE COMPLEMENT DECAV-ACCELERATING FACTOR PRECURSOR.
GN DAF.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HARTLEY; TISSUE-SPLEEN;
RX MEDLINE-95403978; PUBMED-7345710;
RA Nonaka M., Miwa T., Okada N., Nonaka M., Okada H.;
RT Multiple isoforms of guinea pig decay-accelerating factor (DAF)
RT generated by alternative splicing.;
RT J. Immunol. 155:3037-3048(1995).
CC - FUNCTION: PREVENTS THE FORMATION AND/OR ACCELERATES THE
CC - SUBCELLULAR LOCATION: CLASS GPI: ATTACHED TO THE MEMBRANE BY A
CC - GPI-ANCHOR.
CC - ALTERNATIVE PRODUCTS: THERE ARE AT LEAST SIX FORMS OF DAF
CC TRANSCRIPTS (DISTRIBUTED IN FOUR CLASSES: GPI, TCL, TCS AND SEC)
CC GENERATED BY ALTERNATIVE SPLICING. ONE GPI-ANCHORED FORM (GDAB-
CC GPI), TWO FORMS WITH LONGER CYTOPLASMIC REGION (GDAB-TCL AND
CC GDAB-TCS), TWO FORMS WITH SHORTER CYTOPLASMIC REGION (GDA-TCS AND
CC GDA-TS) AND ONE SECRETED FORM (GDAB-SEC).
CC - TISSUE SPECIFICITY: ALL THE ISOFORMS ARE WIDELY EXPRESSED. GPI AND
CC TCS ARE THE MAJOR FORMS, WHEREAS SEC IS MINOR AND TCL IS ONLY

CC PRESENT IN TRACE LEVELS.
CC - SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS
CC - SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
CC (RCA) FAMILY.
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CC or send an email to license@isb-sib.ch).
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CC EMBL: D56035; BAA09514.1; JOINED.
CC EMBL: D56036; BAA09514.1; JOINED.
CC EMBL: D56037; BAA09514.1; JOINED.
CC EMBL: D56038; BAA09514.1; JOINED.
CC EMBL: D56039; BAA09514.1; JOINED.
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CC EMBL: D56044;


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Query Match          33.0%; Score 364.5; DB 1; Length 610;
Best Local Similarity 38.5%; Pred. No. 4,1e-26;
Matches 74; Conservative 31; Mismatches 78; Indels 9; Gaps 3;

OY      3 CNAPEMLPFARNTLTDEEFPIGTLYLVNECPRG--SGRPSPISICLKNSVTGAKDRCR 60
DB      50 CGIPFYLOFPAPFINLNETRFETGTLRTCTCPGRISRKNKFLICDGDGNKK-YKEFCV 108
OY      61 RKSCRNPPDPVNGWNVHVIKGIOFGSQIKRYSCTKGYRLIGSSATCIISGDIYIMDNTPPI 120
DB      109 KKRCENPPELLNGGVIVTVDYFSGESEIEPSCSEGVLIGSANSYCOLQDKGVMSDPLPQ 168
OY      121 CDRIICGLPTPIANDDFISREYTHYGSVYVTHCNLSRGKKVVELGVEPSIYTCKSD 180
DB      169 CIIAKCEPPPTSLNRHNGDEDEFTYGSVTVSCD-----RDFSMLGKASISCREVENK 222
OY      181 QVGINSGPAPOC 192
DB      223 TIGVWSPSPSC 234

RESULT 9
AC      CR2_MOUSE STANDARD: PRT, 1025 AA.
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      01-FEB-1996 (Rel. 33, Last annotation update)
DE      COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).
GN      CR2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BALB/C;
RX      MEDLINE=90229735; PubMed=2139457;
RA      Flingeroh J.D.;
RT      "Comparative structure and evolution of murine CR2. The homolog of
RL      the human C3d/EBV receptor (CD21).";
RL      J. Immunol. 144:3458-3467(1990).
RN      [2]
RP      SEQUENCE OF 12-1025 FROM N.A.
RC      MEDLINE=91010789; PubMed=2145366;
RX      Molina H., Kinoshita T., Inoue K., Carel J.C., Holers V.M.;
RA      "A molecular and immunochemical characterization of mouse CR2.
RT      Evidence for a single gene model of mouse complement receptors 1 and
RL      2.";
RL      J. Immunol. 145:2974-2983(1990).
RN      [3]
RP      SEQUENCE OF 343-401 AND 991-1025 FROM N.A.
RC      MEDLINE=89098890; PubMed=2783485;
RX      Flingeroh J.D., Benedict M.A., Levy D.N., Strominger J.L.;
RA      "Identification of murine complement receptor type 2.";
RT      Proc. Natl. Acad. Sci. U.S.A. 86:242-246(1989).
RN      RN
RP      SEQUENCE OF 289-1025 FROM N.A.
RC      MEDLINE=89381350; PubMed=2528587;
RX      Kutiz C.B., Paul M.S., Aegeerter M., Wels J.J., Wels J.H.;
RA      "Murine complement receptor gene family. II. Identification and
RT      characterization of the murine homolog (Cr2) to human CR2 and its
RL      molecular linkage to Cr1.";
RL      J. Immunol. 143:2058-2067(1989).
RN      RL
RP      FUNCTION: RECEPTOR FOR COMPLEMENT C3D. PARTICIPATES IN B
CC      LYMPHOCYTES ACTIVATION.
CC      -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1 TISSUE SPECIFICITY: B LYMPHOCYTES.
CC      -1 SIMILARITY: TO HUMAN C3D/EBV RECEPTOR (CD21).
CC      -1 SIMILARITY: CONTAINS 15 SUSHI (SCR) REPEATS.
CC      CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 851 851 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 901 901 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 289 291 YGS -> EER (IN REF. 4).
FT CONFLICT 306 306 S -> T (IN REF. 2).
FT CONFLICT 520 520 P -> A (IN REF. 2).
FT CONFLICT 962 963 MISSING (IN REF. 4).
SO SEQUENCE 1025 AA; 112994 MW; 19E51B9A0273694 CRC64;

Query Match 30.4%; Score 335.5; DB 1; Length 1025;
Best Local Similarity 33.9%; Pred. No. 3.3e-23;
Matches 74; Conservative 27; Mismatches 86; Indels 31; Gaps 6;

QY 3 CNAME-WLPFARPTNLDEFEFPY-----CTYLNECRPGY- 37
DB 124 CQANEMWPTLP--VCESDPLECPSLPTINGHHTGQHVDFVAGLSTVYSCPEYL 180
QY 38 -SGRPSIICIKNSVWTGAKDRCKRSCNDPPVNGVYHIKIOFGSQIKSTCKYR 96
DB 181 LTGKK-TIKCIGSSGDMGVITCKEAOCHKFPNGVKREPLAQVTTVYFSCNEGY 239
QY 97 LIGSSAFCTISGPTVWNETPTICDIPGLPTIANGDFTSISREYHYGVVYHCN 156
DB 240 LQGPSSQCVIEQKAIM-TKKPVCKELCPPPVRNMGSGTSENVKGYSTVYTC 298
QY 157 LGSRGKVFELVEGSESYCTSKDOVGIWSPAPQCI 194
DB 299 PSEPKGVSTLIGEKITICTIGSQRTGIMSGPAPCVL 336

RESULT 10
CABP_MOUSE STANDARD; PRT; 469 AA.
ID CABP_MOUSE
AC P08607;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CAB-BINDING PROTEIN PRECURSOR (CABP).
GN CABPA OR CABP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88024997; PubMed=3663616;
RA Kristensen T., Ogata R.T., Chung L.P., Reid K.B.M., Tack B.F.;
RT "CDNA structure of murine Cab-binding protein, a regulatory component
RT of the serum complement system.";
RL Biochemistry 26:4668-4674(1987).
CC -1- FUNCTION: CABP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT
CC ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR
CC (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT
CC ALSO ACCELERATES THE DEGRADATION OF THE C4B2A COMPLEX (C3
CC CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA
CC CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.
CC -1- SUBUNIT: HOMOPOLYMER. NOT COVALENTLY LINKED. MOUSE LACKS THE
CC BETA CHAIN OF CABP.
CC -1- SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
CC -1- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M17122; AAA37312.1; ALT_INIT.
DR PIR; A27117; NEMSC4.
DR HSSP; P10998; IYVC.
DR MGI; MGI:88229; CABP.
DR INTERPRO; IPR000436; -.
DR PRAM; PR00084; sush1; 6.
KW Complement pathway; Plasma; Glycoprotein; Repeat; Sush1; Signal.
FT SIGNAL 1
FT CHAIN 57 469 CAB-BINDING PROTEIN.
FT DOMAIN 57 414 6 X SUSHI (SCR) REPEATS.
FT REPEAT 57 116 SUSHI 1.
FT REPEAT 119 177 SUSHI 2.
FT REPEAT 180 241 SUSHI 3.
FT REPEAT 244 300 SUSHI 4.
FT REPEAT 302 356 SUSHI 5.
FT REPEAT 358 414 SUSHI 6.
FT DISULFID 58 103 BY SIMILARITY.
FT DISULFID 88 115 BY SIMILARITY.
FT DISULFID 120 160 BY SIMILARITY.
FT DISULFID 146 176 BY SIMILARITY.
FT DISULFID 181 223 BY SIMILARITY.
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FT DISULFID 245 287 BY SIMILARITY.
FT DISULFID 273 299 BY SIMILARITY.
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FT DISULFID 359 400 BY SIMILARITY.
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FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 428 428 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 469 AA; 51551 MW; 41E137CB8DB6C321 CRC64;

Query Match 29.5%; Score 325.5; DB 1; Length 469;
Best Local Similarity 37.1%; Pred. No. 1.2e-22;
Matches 72; Conservative 31; Mismatches 78; Indels 13; Gaps 6;

QY 2 CQANPEWLPFARPTNLDEFEFPYIGTYLNYECRGYSGRPS---IICKNSVWTGAKDR 58
DB 57 KCGPPPALPNLPSADVVRITDFESHRTLTLYCPLRGY-GRGISRMVYCKPGEWE-ISVS 114
QY 59 CRRKSCRNPDPVNGVYVIRKIOFGSQIKSTCKRGLISSASATCIISGDTVIWNET 118
DB 115 CAKHCHRPGLDNGYVNG-ETITFGSQTIERSCDGLFVGSSTSSCEVRRKGVAMSNPF 173
QY 119 PICDRIPGCLPPTIANGDFTSISREYHYGVVYHCNLSRGKRVDELVEPSIYCTSR 178
DB 174 PECYIVKRGPPDISNGHSG-TEDFVYNYNGISYTDOPG-----FRLVGSFPIGCTIV 226
QY 179 DDQVGIWSPAPQC 192
DB 227 NKTVPVWSSSPTPC 240

RESULT 11
CABP_HUMAN STANDARD; PRT; 597 AA.
ID CABP_HUMAN
AC P04003;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)

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DE C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
 DE (PRP).
 GN C4BPA OR C4BP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER.
 RA MEDLINE-90073699; PubMed-2590215;
 RA Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y.;
 RT "Molecular cloning of the cDNA coding for proline-rich protein (PRP):
 RT identity of PRP as C4b-binding protein.";
 RL Biochem. Biophys. Res. Commun. 165:138-144(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-91113199; PubMed-1989602;
 RA Aso T., Okamura S., Matsuguchi T., Sakamoto N., Sata T., Niho Y.;
 RT "Genomic organization of the alpha chain of the human C4b-binding
 RT protein gene.";
 RL Biochem. Biophys. Res. Commun. 174:222-227(1991).
 RN [3]
 RP SEQUENCE OF 9-81 FROM N.A.
 RA MEDLINE-88242821; PubMed-3378624;
 RA Linlin S.J., Lewin A.R., Reid K.B.M.;
 RT "Derivation of the sequence of the signal peptide in human
 RT C4b-binding protein and interspecies cross-hybridisation of the C4bp
 RT cDNA sequence.";
 RL FEBS Lett. 232:328-332(1988).
 RN [4]
 RP SEQUENCE OF 203-288 FROM N.A.
 RA MEDLINE-86301119; PubMed-3017751;
 RA Linlin S.J., Reid K.B.M.;
 RT "Studies on the structure of the human C4b-binding protein gene.";
 RL FEBS Lett. 204:77-81(1986).
 RN [5]
 RP SEQUENCE OF 80-597 FROM N.A.
 RA MEDLINE-86025405; PubMed-3840370;
 RA Chung L.P., Bentley D.R., Reid K.B.M.;
 RT "Molecular cloning and characterization of the cDNA coding for C4b-
 RT binding protein, a regulatory protein of the classical pathway of the
 RT human complement system.";
 RL Biochem. J. 230:133-141(1985).
 RN [6]
 RP SEQUENCE OF 49-88.
 RA MEDLINE-85296001; PubMed-4033666;
 RA Chung L.P., Gagnon J., Reid K.B.M.;
 RT "Amino acid sequence studies of human C4b-binding protein: N-terminal
 RT sequence analysis and alignment of the fragments produced by limited
 RT proteolysis with chymotrypsin and the peptides produced by cyanogen
 RT bromide treatment.";
 RL Mol. Immunol. 22:427-435(1985).
 RN [7]
 RP ELECTRON MICROSCOPY, 3-DIMENSIONAL STRUCTURE, AND LIGAND BINDING.
 RA MEDLINE-83221615; PubMed-6222381;
 RA Dahlback B., Smith C.A., Mueller-Eberhard H.J.;
 RT "Visualization of human C4b-binding protein and its complexes with
 RT vitamin K-dependent protein S and complement protein C2a.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3461-3465(1983).
 CC -1- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT
 CC ACTIVATION. IT BINDS AS A COFACTOR TO C3b/C4b INACTIVATOR
 CC (C3bINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4b. IT
 CC ALSO ACCELERATES THE DEGRADATION OF THE C4bC2a COMPLEX (C3
 CC CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2a. ALPHA
 CC CHAIN BINDS C4b. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S
 CC AND WITH SERUM AMLOID P COMPONENT.
 CC -1- SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS
 CC OF 3 POSSIBLE SORTS: A 570 KDA COMPLEX OF 7 ALPHA CHAINS AND 1
 CC BETA CHAIN, A 530 KDA HOMOPOLYMER OF ALPHA CHAINS OR A 500 KDA
 CC COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN. THE CENTRAL BODY OF
 CC THE ALPHA CHAIN HOMOPOLYMER SUPPORTS TENTACLES, EACH WITH THE
 CC BINDING SITE FOR C4b AT THE END.
 CC -1- TISSUE SPECIFICITY: CHYLOMICRONS IN THE PLASMA.

CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
 CC -1- SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
 CC -----
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 CC -----
 DR EMBL: M31452; AAA36507.1; -;
 DR EMBL: M62486; AAA36506.1; -;
 DR EMBL: M62475; AAA36506.1; JOINED.
 DR EMBL: M62476; AAA36506.1; JOINED.
 DR EMBL: M62477; AAA36506.1; JOINED.
 DR EMBL: M62478; AAA36506.1; JOINED.
 DR EMBL: M62479; AAA36506.1; JOINED.
 DR EMBL: M62480; AAA36506.1; JOINED.
 DR EMBL: M62481; AAA36506.1; JOINED.
 DR EMBL: M62482; AAA36506.1; JOINED.
 DR EMBL: M62484; AAA36506.1; JOINED.
 DR EMBL: M62485; CAA30701.1; -;
 DR EMBL: X07853; CAA30701.1; -;
 DR EMBL: X04284; CAA31244.1; -;
 DR EMBL: X04296; CAA27839.1; -;
 DR EMBL: X02865; CAA26617.1; -;
 DR PIR: A33568; NBHUC4.
 DR HSSP: P10998; LYVC.
 DR MIM: 120830; -;
 DR INTERPRO: IPR000436; -;
 DR PFM: PF00084; sush1; 8.
 KW Complement pathway; Plasma; Glycoprotein; Repeat; Sushi; Signal;
 KW Polymorphism.
 FT STGNAL 1 48
 FT CHAIN 49 597
 FT DOMAIN 49 539
 FT REPEAT 49 109
 FT REPEAT 112 171
 FT REPEAT 174 235
 FT REPEAT 238 295
 FT REPEAT 298 361
 FT REPEAT 364 423
 FT REPEAT 425 481
 FT REPEAT 483 539
 FT DISULFID 50 96
 FT DISULFID 81 108
 FT DISULFID 113 154
 FT DISULFID 140 170
 FT DISULFID 175 217
 FT DISULFID 203 234
 FT DISULFID 239 281
 FT DISULFID 267 294
 FT DISULFID 299 348
 FT DISULFID 332 360
 FT DISULFID 7364 7387
 FT DISULFID 7365 7409
 FT DISULFID 7399 422
 FT DISULFID 426 468
 FT DISULFID 454 480
 FT DISULFID 484 525
 FT DISULFID 511 538
 FT DISULFID 546 546
 FT DISULFID 558 558
 FT CARBOHYD 221 221
 FT CARBOHYD 506 506
 FT CARBOHYD 528 528
 FT VARIANT 92 92
 FT VARIANT 357 357
 FT SEQUENCE 597 AA; 67033 MM; 67E03FE2E85A10DD CRC64;
 /FRI4-VAR_001978.
 Y -> H.
 Q -> T.
 N-LINKED (GLCNAC. . .).
 N-LINKED (GLCNAC. . .).
 N-LINKED (GLCNAC. . .).
 O -> T.
 Y -> H.
 /FRI4-VAR_001978.
 67E03FE2E85A10DD CRC64;


```

FT VARSPLIC 286 300 MISSING (IN A SECOND FORM).
FT VARSPLIC 340 352 MISSING (IN ISOFORM M).
FT VARSPLIC 353 361 YLRRKKKG -> DIERGRRKQWELMPLTRLNPLQ
FT VARSPLIC 362 377 OSREAE (IN ISOFORM M).
FT VARSPLIC 362 377 TYLDELHREKFTSL -> KADGAEVATYQKSTTPAQ
FT VARSPLIC 362 377 RG (IN ISOFORM B/D/E/H/J/L).
FT VARSPLIC 362 377 MISSING (IN ISOFORM M AND ISOFORM N).
FT VARSPLIC 340 361 MISSING (IN ISOFORM N).
FT VARSPLIC 339 339 I -> IGKQWELMPLTRLNPLQOSREAE (IN
SQ SEQUENCE 377 AA: 42247 MW: 2CA6F61752570B57 CRC64;
ISOFORM N).

Query Match 26.7%; Score 295; DB 1; Length 377;
Best Local Similarity 36.0%; Pred. No. 5; 9e-20;
Matches 63; Conservative 25; Mismatches 77; Indels 10; Gaps 5;

OY 23 FPIGTLYNCRPGYSGRP---FSIICKNSVWTC-AKDRCRKSCNPPDPVNGWHVI 78
DB 54 YELGERDYCKKGYFIPLPLATHTICDRNHTWLPVSDDACRYETCPIYRDLGQAVPA 113
OY 79 KG-IQFSSQIKYSCTKGYRLIGSSSACIISGDTVIMDNETPICDRIPCGLPIIANGDF 137
DB 114 NGTYEFYQHFICNEGYLIGEEILYCELKGSVAIMSGKPICEKYLCPPEPKIKNGKH 173
OY 138 TTSISREYFHGYSVTYHCNIGSRGKVFELVGEPSIYCTSKDOVGWISGPAPOC 192
DB 174 TFESEVEFYELDAVTYSCD-PAPGPDPFSLIGESTIYCGDN---SVMSRAAPPC 223

RESULT 13
CCPH_HSVSA
ID CCPH_HSVSA STANDARD; PRT; 360 AA.
AC 001016;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE COMPLEMENT CONTROL PROTEIN HOMOLOG PRECURSOR (CCPH).
GN 4 OR CCPH.
OS Herpesvirus saimiri (strain 11).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333688; PubMed=1321287;
RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
RA Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
RA Honess R.W.;
RT "Primary structure of the herpesvirus saimiri genome.";
RL J. Virol. 66:5047-5058(1992).
RN [2]
RP SIMILARITY TO CCP.
RX MEDLINE=92260674; PubMed=1316492;
RA Albrecht J.-C., Fleckenstein B.;
RT "New member of the multigene family of complement control proteins in
herpesvirus saimiri."
RL J. Virol. 66:3937-3940(1992).
CC -|- ALTERNATIVE PRODUCTS: A MEMBRANE-BOUND FORM AND A SECRETED FORM
CC ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
CC -|- SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF
CC COMPLEMENT ACTIVATION (RCA).
CC -|- SIMILARITY: CONTAINS 3 SUSHI (SCR) REPEATS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
DR EMBL: X64346; CAA45626.1; -
DR EMBL: X64346; CAA45627.1; -

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DR EMBL: X60283; CAA42823.1; -
DR EMBL: X60283; CAA42822.1; -
DR PIR: B42534; WMBE2E.
DR PIR: A42534; WMBE1E.
DR PIR: S24567; S24567.
DR HSSP: P10998; 1VVC.
DR INTERPRO: IPR000436; -
DR PRAM: PF00084; sushi; 4.
KW Signal; Repeat; Sushi; Transmembrane; Alternative splicing;
KW Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 360
FT DOMAIN 83 265
FT REPEAT 83 143
FT REPEAT 146 206
FT REPEAT 209 265
FT TRANSMEM 328 350
FT DISULFID 84 125
FT DISULFID 111 142
FT DISULFID 147 191
FT DISULFID 175 205
FT DISULFID 210 252
FT DISULFID 238 264
FT CARBOHYD 36 36
FT CARBOHYD 39 39
FT CARBOHYD 46 46
FT CARBOHYD 72 72
FT CARBOHYD 155 155
FT CARBOHYD 294 294
FT VARSPLIC 289 302
FT VARSPLIC 303 360
SQ SEQUENCE 360 AA: 40006 MW: 6278A6C2ECD49669 CRC64;
MISSING (IN SHORT ISOFORM).

Query Match 26.4%; Score 292; DB 1; Length 360;
Best Local Similarity 36.1%; Pred. No. 1; 1e-19;
Matches 66; Conservative 27; Mismatches 70; Indels 20; Gaps 7;

OY 16 NLAD-EPEFPIGTLYNCRPGYSGRPFSIICKNSVWTCAGKRCRKRSCNPPDPVNGM 74
DB 36 NLNYSGPYNGTTLHTLHTCDEGYAKRPVQVTCVNGWMTYPR-KCQKKKSTPDLLNGR 94
OY 75 VHVIKGIQFSSQIKYSCTKGYRLIGSSSACIIS-GDTVIMDNETPICDRIPCGLPII 133
DB 95 YTVAGNLYGVSIVTYTCNSGSLIGSTTACILKRGGRVDMTPPICDIKKCKPPQIA 154
OY 134 NGDPTTSISREYFHGYSVTYHCNIGSRGKVFELVGEPSIYCTSKDOVGWISGPAPOC 193
DB 155 NGHTNV-KDFYTYLDTVTYSCN---DETKTLTGPSSKICS---ETGSM----- 197
OY 194 IPN 196
DB 198 VFN 200

RESULT 14
CR2_HUMAN
ID CR2_HUMAN STANDARD; PRT; 1033 AA.
AC P20023;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR)
DE (EPSREIN-BARR VIRUS RECEPTOR) (CD21 ANTIGEN).
GN CR2 OR C3DR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89123277; PubMed=2563370;
RA Fujisaku A., Harley J.B., Frank M.B., Gruner B.A., Frazier B.,

```

Query Match	Best Local Similarity	Score	DB 1	Length	1033
Matches 75, Conservative 18, Mismatches 87, Indels 35, Gaps 8,	26.3%;	290.5;	DB 1;	Length 1033;	
1	MOCANP-EMLEFA-----RPTNLD-----EFFFPIGTLYNTYCRPGY--SGRPF	42			
391	IRCNAGCTWESAPVCEKECAPPILNGOEDRHMRVFDGTSIKYSCNPGYLVGEE-	449			
43	SIILKNSVWFAGDKRCRKRSCRPN-----DDPVAGVNHVKGIDFGSQIKYSCKRGYRL	97			
450	SIQCTSESVWTPPVYPCQCVACACATGRGLLTKRFQHQFTR-----PDVNSSCGEGYKL	501			
98	IGSSATCIIISGDVIYVMDNETPFCODRIPLCGLPPTIANGDFTSISREYHYGSVYVYHCNL	157			
502	SGSYVOEC---QGTIPIWFMETRLCKEITCPCPPPIYVNGAHGSSLEDPRPGTYVYTCNP	558			
158	GSRGKVFELVINGEBSICTSKDDQVGTMSGAPQC	192			

DB 559 GPERGVFSLIGESTIRCTSDNGERTWGSAPLIC 593

RESULT 15

VCP_VACCV STANDARD; PRT; 263 AA.

AC P10998:

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE COMPLEMENT CONTROL PROTEIN PRECURSOR (VCP) (SECRETORY PROTEIN 35)

DE (PROTEIN C3) (28 KDA PROTEIN).

GN C3L.

OS Vaccinia virus (strain WR), and Vaccinia virus (strain Copenhagen).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OC [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-37.

RC STRAIN-WR:

RX MEDLINE=88318974; PubMed=3412473;

RA Kotwal G.J., Moss B.;

RT "Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins.";

RL Nature 335:176-178(1988).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-WR:

RX MEDLINE=89073756; PubMed=2849238;

RA Kotwal G.J., Moss B.;

RT "Analysis of a large cluster of nonessential genes deleted from a vaccinia virus terminal transposition mutant.";

RL Virology 167:524-537(1988).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-COPENHAGEN:

RX MEDLINE=91021027; PubMed=2219722;

RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P., Paoletti E.;

RT "The complete DNA sequence of vaccinia virus.";

RL Virology 179:247-266(1990).

RN [4]

RP COMPLETE GENOME.

RC STRAIN-COPENHAGEN:

RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P., Paoletti E.;

RL Virology 179:517-563(1990).

RN [5]

RP FUNCTION.

RX MEDLINE=92115714; PubMed=1731333;

RA Isaacs S.N., Kotwal G.J., Moss B.;

RT "Vaccinia virus complement-control protein prevents antibody-dependent complement-enhanced neutralization of infectivity and contributes to virulence.";

RL Proc. Natl. Acad. Sci. U.S.A. 89:628-632(1992).

RN [6]

RP STRUCTURE BY NMR OF 146-263.

RX MEDLINE=97446168; PubMed=9299352;

RA Wiles A.P., Shaw G., Bright J., Perczel A., Campbell I.D., Barlow P.N.;

RT "NMR studies of a viral protein that mimics the regulators of complement activation.";

RL J. Mol. Biol. 272:253-265(1997).

CC -I- FUNCTION: SERVES TO PROTECT THE VIRUS AGAINST COMPLEMENT ATTACK BY INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF COMPLEMENT ACTIVATION. BINDS C3B AND C4B.

CC -I- SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).

CC -I- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.

CC -----

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CC -----

DR EMBL; X13166; CAA31564.1; -

DR EMBL; M22812; AAA69605.1; -

DR EMBL; M35027; AAA47997.1; -

DR PIR; A31005; MWVZSP.

DR PDB; 1VVC; 03-DEC-97.

DR PDB; 1VVD; 03-DEC-97.

DR PDB; 1VVE; 03-DEC-97.

DR INTERPRO: IPR000436; -

DR PFM; PF00084; sush1; 4

KW Signal; Repeat; Sush1; 3D-structure.

FT SIGNAL 1 19

FT CHAIN 20 263

FT DOMAIN 20 262

FT REPEAT 20 82

FT REPEAT 85 144

FT REPEAT 147 202

FT REPEAT 205 262

FT DISULFID 21 70

FT DISULFID 54 81

FT DISULFID 86 126

FT DISULFID 112 143

FT DISULFID 148 190

FT DISULFID 176 201

FT DISULFID 206 248

FT DISULFID 234 261

SO SEQUENCE 263 AA; 28629 MM; E4322CC9A6EF997 CRC64;

COMPLEMENT CONTROL PROTEIN.

4 x SUSHI (SCR) REPEATS.

SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 4.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

Query Match 26.1%; Score 288.5; DB 1; Length 263;

Best Local Similarity 35.0%; Pred. No. 1.6e-19;

Matches 71; Conservative 30; Mismatches 71; Indels 31; Gaps 11;

QY 3 CNAPEWLPFARPTNL-----TD-EFEPIGTLYNTECRPRYSGRPFSLCLK--NSW 52

DB 21 CQIP-----SRPINKMKFNKSVETDANANNYIGDTLEYLCLPGRKQKMPYAKCTGTGW 75

QY 53 TGAKDRRCRRKSCRNPPDPVNGWVHVKIGFQSOIKYSCCTKGRILGSSATCII-SCGT 111

DB 76 T-LFNOCIRRRPSPPDINDGOLD-IGVDFFSSITSCNSGHLIGESKSTCELASTGS 133

QY 112 VYWDNETPICDRIPGCLPTIANGDFTSISREYFHGSVVYVHCNIGSRGKVFELVGP 171

DB 134 MVMNPEAPICESVKQSPSISNGRHNG-EDFYTGDSVVTYSCNSG-----YSLIGNS 186

QY 172 STYCTSKDQVGIVSGPAPQCII 194

DB 187 GVLCSG-----GEWSDP-PTCOI 203

Search completed: January 13, 2001, 13:47:40

UO time: 385 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2001, 13:42:36 ; Search time 73.65 Seconds
(without alignments)
313.509 Million cell updates/sec

Title: US-09-380-682-1
Perfect score: 1104
Sequence: 1 MGNAPWLPFARPTNLDE.....KDDQVGTWSPAPCIIPIPK 197

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_PISCES:*
8: SP_ORNITHES:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1042	94.4	559	4	Q9UOV2
2	1042	94.4	2039	4	Q16745
3	1042	94.4	2489	4	Q16744
4	1029	93.2	661	6	Q29531
5	1029	93.2	2014	6	Q29530
6	946	85.7	522	6	Q28769
7	937	84.9	522	6	Q28797
8	923	83.6	315	6	Q28770
9	780	70.7	1911	6	Q29528
10	702	63.6	483	11	Q64735
11	689	62.4	497	11	Q63612
12	689	62.4	559	11	Q63135
13	681	61.7	162	4	Q9UOR7
14	624	56.5	679	11	Q99254
15	474	42.9	330	11	Q62479
16	410	37.1	305	6	Q9MYJ3
17	410	37.1	347	6	Q9MYJ6
18	409	37.0	347	6	Q9MYJ7
19					Q9MYJ7 gorilla gor

20	407	36.9	347	4	P78361	P78361 homo sapien
21	406	36.8	271	6	Q9MYJ0	Q9MYJ0 erythrocebu
22	406	36.8	278	6	Q9MYJ1	Q9MYJ1 erythrocebu
23	406	36.8	343	6	Q9MYJ2	Q9MYJ2 erythrocebu
24	406	36.8	343	6	Q9MYJ2	Q9MYJ2 erythrocebu
25	405	36.7	343	6	Q9MYJ4	Q9MYJ4 papio hamad
26	399	36.1	257	11	Q61447	Q61447 mus musculu
27	375	34.0	363	6	Q02839	Q02839 sus scrofa
28	366	33.2	180	11	Q60400	Q60400 cavia porce
29	364.5	33.0	383	11	Q9WT19	Q9WT19 cavia porce
30	363	32.9	372	11	Q9QYJ9	Q9QYJ9 rattus norv
31	363	32.9	382	11	Q9QUM3	Q9QUM3 rattus norv
32	363	32.9	399	11	Q9QUM6	Q9QUM6 rattus norv
33	363	32.9	399	11	Q9QUM6	Q9QUM6 rattus norv
34	363	32.9	466	11	Q92019	Q92019 rattus norv
35	353	32.0	533	11	Q35520	Q35520 rattus norv
36	353	32.0	533	11	Q08569	Q08569 cavia porce
37	344	31.2	89	11	Q63129	Q63129 rattus norv
38	342.5	31.0	579	11	Q60736	Q60736 mus musculu
39	311	28.2	645	12	Q9WRU2	Q9WRU2 macaca mula
40	306	27.7	1045	6	Q46545	Q46545 ovis aries
41	299.5	27.1	377	6	Q62837	Q62837 saguinus oe
42	299.5	27.1	378	6	Q62837	Q62837 saguinus oe
43	295	26.7	349	4	Q15429	Q15429 homo sapien
44	293.5	26.6	395	12	Q9J2M6	Q9J2M6 macaca mula
45	292.5	26.5	285	6	Q19121	Q19121 papio hamad

ALIGNMENTS

```

RESULT 1
ID Q9UOV2 PRELIMINARY; PRT; 559 AA.
AC Q9UOV2:
DT 01-MAY-2000 (TEMBREL. 13, Created)
DT 01-OCT-2000 (TEMBREL. 15, Last annotation update)
DE HUMAN CRI MRNA FOR C3B/C4B RECEPTOR SECRETED FORM PRECURSOR
DE (FRAGMENT).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010527; Pubmed=2971757;
RA Hourcade D., Miesner D.R., Atkinson J.P., Hoiers V.M.;
RT C3b/C4b receptor (complement receptor type 1) transmembrane unit and
RT Prediction of a secreted form of complement receptor type 1.
RL J. Exp. Med. 168:1255-1270(1988).
DR EMBL: X14362; CAA32541.1; -.
DR HSP: P10998; IVD.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000834; -.
DR INTERPRO: IPR002396; -.
DR PIRAM: PFO0084; Sush1; 8.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00133; CARBOXYPEPT_2N_2; UNKNOWN_1.
KW SIGNAL.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 17 559 POTENTIAL.
FT CHAIN 17 559 POTENTIAL.
SO SEQUENCE 559 AA; 61424 MW; DBFPE955CA179D75 CRC64;

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Query Match 94.4%; Score 1042; DB 4; Length 559;
Best Local Similarity 94.9%; Pred. No. 9.7e-101;
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Db 17 OCNABEWLPFARPTNLDEFEFFPIGTLYNTECRPGYSGRPSITCLKNKSVTGAKDCRR 76
QY 62 KSCRNPDPVNGMVHVIGKIGFGSQIKYKSCYKGYRLIGSSSATCIIISGDTYIMDNETPIC 121
Db 77 KSCRNPDPVNGMVHVIGKIGFGSQIKYKSCYKGYRLIGSSSATCIIISGDTYIMDNETPIC 136
QY 122 DRIPGGLPPTIANGDFTSISREYFHGYSVVTYHGNLGSRGKRVFELVGEPSIYCTSKDDQ 181
Db 137 DRIPGGLPPTIANGDFTSISREYFHGYSVVTYHGNLGSRGKRVFELVGEPSIYCTSKDDQ 196
QY 182 VGWISGPAPQCIIPNK 197
Db 197 VGWISGPAPQCIIPNK 212

RESULT 2
016745 PRELIMINARY: PRT: 2039 AA.
ID 016745
AC 016745.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COMPLEMENT RECEPTOR 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94065175; PubMed=8245463;
RA Vik D.P., Wong W.W.;
RT "Structure of the gene for the F allele of complement receptor type 1
and sequence of the coding region unique to the S allele.";
RL J. Immunol. 151:6214-6224(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Vik D.P., Wong W.W.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: L17418; AAB60694.1; JOINED.
DR EMBL: L17390; AAB60694.1; JOINED.
DR EMBL: L17391; AAB60694.1; JOINED.
DR EMBL: L17392; AAB60694.1; JOINED.
DR EMBL: L17393; AAB60694.1; JOINED.
DR EMBL: L17394; AAB60694.1; JOINED.
DR EMBL: L17395; AAB60694.1; JOINED.
DR EMBL: L17396; AAB60694.1; JOINED.
DR EMBL: L17397; AAB60694.1; JOINED.
DR EMBL: L17398; AAB60694.1; JOINED.
DR EMBL: L17399; AAB60694.1; JOINED.
DR EMBL: L17400; AAB60694.1; JOINED.
DR EMBL: L17401; AAB60694.1; JOINED.
DR EMBL: L17402; AAB60694.1; JOINED.
DR EMBL: L17403; AAB60694.1; JOINED.
DR EMBL: L17404; AAB60694.1; JOINED.
DR EMBL: L17405; AAB60694.1; JOINED.
DR EMBL: L17406; AAB60694.1; JOINED.
DR EMBL: L17407; AAB60694.1; JOINED.
DR EMBL: L17408; AAB60694.1; JOINED.
DR EMBL: L17409; AAB60694.1; JOINED.
DR EMBL: L17410; AAB60694.1; JOINED.
DR EMBL: L17411; AAB60694.1; JOINED.
DR EMBL: L17412; AAB60694.1; JOINED.
DR EMBL: L17413; AAB60694.1; JOINED.
DR EMBL: L17414; AAB60694.1; JOINED.
DR EMBL: L17415; AAB60694.1; JOINED.
DR EMBL: L17416; AAB60694.1; JOINED.
DR EMBL: L17417; AAB60694.1; JOINED.
DR EMBL: L17419; AAB60694.1; JOINED.
DR EMBL: L17420; AAB60694.1; JOINED.
DR EMBL: L17421; AAB60694.1; JOINED.
DR EMBL: L17422; AAB60694.1; JOINED.
DR EMBL: L17423; AAB60694.1; JOINED.
HSP; P08603; IHLI.

DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000834; -.
DR INTERPRO: IPR001424; -.
DR PFAM: PF00084; sushi; 30.
DR PROSITE: PS00087; SOD_CU_ZN_1; UNKNOWN_1.
DR PROSITE: PS00133; CARBOXYEPT_ZN_2; UNKNOWN_2.
SQ SEQUENCE 2039 AA; 223603 MW; B82FCB1166B16635 CRC64;

Query Match 94.4%; Score 1042; DB 4; Length 2039;
Best Local Similarity 94.9%; Pred. No. 4.8e-100;
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 OCNABEWLPFARPTNLDEFEFFPIGTLYNTECRPGYSGRPSITCLKNKSVTGAKDCRR 61
Db 42 OCNABEWLPFARPTNLDEFEFFPIGTLYNTECRPGYSGRPSITCLKNKSVTGAKDCRR 101
QY 62 KSCRNPDPVNGMVHVIGKIGFGSQIKYKSCYKGYRLIGSSSATCIIISGDTYIMDNETPIC 121
Db 102 KSCRNPDPVNGMVHVIGKIGFGSQIKYKSCYKGYRLIGSSSATCIIISGDTYIMDNETPIC 161
QY 122 DRIPGGLPPTIANGDFTSISREYFHGYSVVTYHGNLGSRGKRVFELVGEPSIYCTSKDDQ 181
Db 162 DRIPGGLPPTIANGDFTSISREYFHGYSVVTYHGNLGSRGKRVFELVGEPSIYCTSKDDQ 221
QY 182 VGWISGPAPQCIIPNK 197
Db 222 VGWISGPAPQCIIPNK 237

RESULT 3
016744 PRELIMINARY: PRT: 2489 AA.
ID 016744
AC 016744.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COMPLEMENT RECEPTOR 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94065175; PubMed=8245463;
RA Vik D.P., Wong W.W.;
RT "Structure of the gene for the F allele of complement receptor type 1
and sequence of the coding region unique to the S allele.";
RL J. Immunol. 151:6214-6224(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Vik D.P., Wong W.W.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: L17418; AAB60695.1; JOINED.
DR EMBL: L17390; AAB60695.1; JOINED.
DR EMBL: L17391; AAB60695.1; JOINED.
DR EMBL: L17392; AAB60695.1; JOINED.
DR EMBL: L17393; AAB60695.1; JOINED.
DR EMBL: L17394; AAB60695.1; JOINED.
DR EMBL: L17395; AAB60695.1; JOINED.
DR EMBL: L17396; AAB60695.1; JOINED.
DR EMBL: L17397; AAB60695.1; JOINED.
DR EMBL: L17398; AAB60695.1; JOINED.
DR EMBL: L17399; AAB60695.1; JOINED.
DR EMBL: L17400; AAB60695.1; JOINED.
DR EMBL: L17401; AAB60695.1; JOINED.
DR EMBL: L17402; AAB60695.1; JOINED.
DR EMBL: L17403; AAB60695.1; JOINED.
DR EMBL: L17405; AAB60695.1; JOINED.
DR EMBL: L17406; AAB60695.1; JOINED.
DR EMBL: L17407; AAB60695.1; JOINED.
DR EMBL: L17408; AAB60695.1; JOINED.
DR EMBL: L17409; AAB60695.1; JOINED.

DR EMBL: L17410: AAB60695.1: JOINED.
DR EMBL: L17411: AAB60695.1: JOINED.
DR EMBL: L17412: AAB60695.1: JOINED.
DR EMBL: L17413: AAB60695.1: JOINED.
DR EMBL: L17414: AAB60695.1: JOINED.
DR EMBL: L17415: AAB60695.1: JOINED.
DR EMBL: L17416: AAB60695.1: JOINED.
DR EMBL: L17417: AAB60695.1: JOINED.
DR EMBL: L17418: AAB60695.1: JOINED.
DR EMBL: L17419: AAB60695.1: JOINED.
DR EMBL: L17420: AAB60695.1: JOINED.
DR EMBL: L17421: AAB60695.1: JOINED.
DR EMBL: L17422: AAB60695.1: JOINED.
DR EMBL: L17423: AAB60695.1: JOINED.
DR EMBL: L17424: AAB60695.1: JOINED.
DR EMBL: L17425: AAB60695.1: JOINED.
DR EMBL: L17426: AAB60695.1: JOINED.
DR EMBL: L17427: AAB60695.1: JOINED.
DR EMBL: L17428: AAB60695.1: JOINED.
DR EMBL: L17429: AAB60695.1: JOINED.
DR EMBL: L17430: AAB60695.1: JOINED.
DR HSSP: P08603: 1HFI.
DR INTERPRO: IPR000436: -.
DR INTERPRO: IPR000834: -.
DR INTERPRO: IPR001424: -.
DR PFAM: PF00084: sush1: 37.
DR PROSITE: PS00087: SOD_CU_ZN_1: UNKNOWN_1.
DR PROSITE: PS00133: CARBOXYPEPT_ZN_2: UNKNOWN_3.
SQ SEQUENCE 2489 AA: 272846 MW: CEE1B53F2B4FAF6 CRC64:

Query Match 94.4% Score 1042: DB 4: Length 2489;
Best Local Similarity 94.9% Pred. No 6.1e-100;
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNAPFWLPEFARPTNLTDEFEPIGTYLNECRPGYSGRPSIICLNKSWTGAKDCRR 61
DB 42 QCNAPFWLPEFARPTNLTDEFEPIGTYLNECRPGYSGRPSIICLNKSWTGAKDCRR 101
QY 62 KSCNRPDPVNGMVHVYKGIQFGSQIKYSGTKGRLIGSSATCIIISGDVIMNENEPIC 121
DB 102 KSCNRPDPVNGMVHVYKGIQFGSQIKYSGTKGRLIGSSATCIIISGDVIMNENEPIC 161
QY 122 DRIPCGLPPTITNGDFISREYHYGSVYVYHGNLGRKGVYELVGEPSIYCTSDQ 181
DB 162 DRIPCGLPPTITNGDFISREYHYGSVYVYHGNLGRKGVYELVGEPSIYCTSDQ 221
QY 182 VGIMSGAPQCIIPNK 197
DB 222 VGIMSGAPQCIIPNK 237

RESULT 4
Q29531 PRELIMINARY; PRT; 661 AA.
AC Q29531:
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DE 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE COMPLEMENT RECEPTOR 1 PRECURSOR (FRAGMENT).
GN CRI.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292799; PubMed=8021505;
RA Birmingham D.J., Shen X.P., Hourcade D., Nickells M.W., Atkinson J.P.;
RT "Primary sequence of an alternatively spliced form of CRI. Candidate
RT for the 75,000 M(r) complement receptor expressed on chimpanzee
RT erythrocytes."
RL J. Immunol. 153:691-700(1994).
DR EMBL: L24921: AAA51439.1: -.
DR

DR HSSP: P10998: 1VVD.
DR INTERPRO: IPR000436: -.
DR INTERPRO: IPR001424: -.
DR INTERPRO: IPR002396: -.
DR PFAM: PF00084: sush1: 9.
DR PRINTS: PR00343: SELECTIN.
DR PROSITE: PS00087: SOD_CU_ZN_1: UNKNOWN_1.
KW Signal; Alternative splicing.
FT NON_TER 1
FT SIGNAL <1 16 POTENTIAL.
FT CHAIN 17 >661 COMPLEMENT RECEPTOR 1.
FT NON_TER 661
SQ SEQUENCE 661 AA: 72966 MW: 3F0DF1532664D3F0 CRC64;

Query Match 93.2% Score 1029: DB 6: Length 661;
Best Local Similarity 93.9% Pred. No 2.7e-99;
Matches 184; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 QCNAPFWLPEFARPTNLTDEFEPIGTYLNECRPGYSGRPSIICLNKSWTGAKDCRR 61
DB 17 QCNAPFWLPEFARPTNLTDEFEPIGTYLNECRPGYSGRPSIICLNKSWTGAKDCRR 76
QY 62 KSCNRPDPVNGMVHVYKGIQFGSQIKYSGTKGRLIGSSATCIIISGDVIMNENEPIC 121
DB 77 KSCNRPDPVNGMVHVYKGIQFGSQIKYSGTKGRLIGSSATCIIISGDVIMNENEPIC 136
QY 122 DRIPCGLPPTITNGDFISREYHYGSVYVYHGNLGRKGVYELVGEPSIYCTSDQ 181
DB 137 DRIPCGLPPTITNGDFISREYHYGSVYVYHGNLGRKGVYELVGEPSIYCTSDQ 196
QY 182 VGIMSGAPQCIIPNK 197
DB 197 VGIMSGAPQCIIPNK 212

RESULT 5
Q29530 PRELIMINARY; PRT; 2014 AA.
AC Q29530:
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DE 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE COMPLEMENT RECEPTOR 1 (FRAGMENT).
GN CRI.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292799; PubMed=8021505;
RA Birmingham D.J., Shen X.P., Hourcade D., Nickells M.W., Atkinson J.P.;
RT "Primary sequence of an alternatively spliced form of CRI. Candidate
RT for the 75,000 M(r) complement receptor expressed on chimpanzee
RT erythrocytes."
RL J. Immunol. 153:691-700(1994).
DR EMBL: L24920: AAA51438.1: -.
DR HSSP: P08603: 1HFI.
DR INTERPRO: IPR000436: -.
DR INTERPRO: IPR000834: -.
DR INTERPRO: IPR001424: -.
DR PFAM: PF00084: sush1: 30.
DR PROSITE: PS00087: SOD_CU_ZN_1: UNKNOWN_1.
DR PROSITE: PS00133: CARBOXYPEPT_ZN_2: UNKNOWN_2.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 2014 AA: 221280 MW: 6D6C3A74D81F1DB9 CRC64;

Query Match 93.2% Score 1029: DB 6: Length 2014;
Best Local Similarity 93.9% Pred. No 1.1e-98;
Matches 184; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

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QY 2 QCNAPFWLPFARPTNLTDEFEPPITGYLYNECRPGYSGRPSIICLKNSVWTGAKDRCR 61
D 17 QCNAPFWLPFARPTNLTDEFEPPITGYLYNECRPGYSGRPSIICLKNSVWTGAKDRCR 76
OY 62 KSCRNPDPVNGMVAVYIGIOFGSOIKYSCRTGKGYRLIGSSSATCIIISDVIWNETPIC 121
D 77 KSCRNPDPVNGMVAVYIGIOFGSOIKYSCRTGKGYRLIGSSSATCIIISDVIWNETPIC 136
OY 122 DRIPGCLPTIANGDFTSISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQ 181
D 137 DRIPGCLPTIANGDFTSISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQ 196
OY 182 VGIWSPAPQCIIPNK 197
D 197 VGIWSPAPQCIIPNK 212

RESULT 6
Q28769 PRELIMINARY: PRT: 522 AA.
AC Q28769:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE COMPLEMENT RECEPTOR (FRAGMENT).
OS Papilio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Birmingham D.J., Logar C.M., Shen X.P., Chen W.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: L77977; AAA99004.1; -.
DR HSSP: P10998; 1YVD.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00084; sush1; 7.
DR PRINTS: PR00343; SELECTIN.
FT NON_TER 1
FT SEQUENCE 522 AA; 56626 MW; 312FCBE03ADF19DC CRC64;

Query Match 85.7%; Score 946; DB 6; Length 522;
Best Local Similarity 87.2%; Pred. No. 9,9e-91;
Matches 171; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 2 QCNAPFWLPFARPTNLTDEFEPPITGYLYNECRPGYSGRPSIICLKNSVWTGAKDRCR 61
D 47 QCNAPFWLPFARPTNLTDEFEPPITGYLYNECRPGYSGRPSIICLKNSVWTGAKDRCR 106
OY 62 KSCRNPDPVNGMVAVYIGIOFGSOIKYSCRTGKGYRLIGSSSATCIIISDVIWNETPIC 121
D 107 KSCRNPDPVNGMVAVYIGIOFGSOIKYSCRTGKGYRLIGSSSATCIIISDVIWNETPIC 166
OY 122 DRIPGCLPTIANGDFTSISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQ 181
D 167 DRIPGCLPTIANGDFTSISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQ 226
OY 182 VGIWSPAPQCIIPNK 197
D 227 VGIWSPAPQCIIPNK 242

RESULT 7
Q28797 PRELIMINARY: PRT: 522 AA.
AC Q28797:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
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DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE UNKNOWN PROTEIN (FRAGMENT).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292799; PubMed=8021505;
RA Birmingham D.J., Shen X.P., Hourcade D., Nickells M.W., Atkinson J.P.;
RT "Primary sequence of an alternatively spliced form of CR1. Candidate
RT for the 75,000 M(r) complement receptor expressed on chimpanzee
RT erythrocytes."
RL J. Immunol. 153:691-700(1994).
DR EMBL: L24922; AAA50460.1; -.
DR HSSP: P10998; 1YVD.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000834; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00084; sush1; 8.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00133; CARBOXYDEPT_2N_2; UNKNOWN_1.
FT NON_TER 1
FT SEQUENCE 522 AA; 57304 MW; DB8456EF462C00C9 CRC64;

Query Match 84.9%; Score 937; DB 6; Length 522;
Best Local Similarity 93.3%; Pred. No. 8,7e-90;
Matches 167; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 19 DEFEPPITGYLYNECRPGYSGRPSIICLKNSVWTGAKDRCRKSCRNPDPVNGMVAVI 78
D 1 DEFEPPITGYLYNECRPGYSGRPSIICLKNSVWTGAKDRCRKSCRNPDPVNGMVAVI 60
OY 79 KGIOFGSOIKYSCRTGKGYRLIGSSSATCIIISDVIWNETPICDRIPGCLPTIANGDFT 138
D 61 KGIOFGSOIKYSCRTGKGYRLIGSSSATCIIISDVIWNETPICDRIPGCLPTIANGDFT 120
OY 139 SISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQYGIWSPAPQCIIPNK 197
D 121 SISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQYGIWSPAPQCIIPNK 179

RESULT 8
Q28770 PRELIMINARY: PRT: 315 AA.
AC Q28770:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE COMPLEMENT RECEPTOR (FRAGMENT).
OS Papilio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Birmingham D.J., Logar C.M., Shen X.P., Chen W.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: L77978; AAA99005.1; -.
DR HSSP: P10998; 1YVD.
DR INTERPRO: IPR000436; -.
DR PFAM: PF00084; sush1; 5.
FT NON_TER 1
FT SEQUENCE 315 AA; 35172 MW; 305B314AE752824F CRC64;

Query Match 83.6%; Score 923; DB 6; Length 315;
Best Local Similarity 84.7%; Pred. No. 1,4e-88;
Matches 166; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
```


DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE 512 ANTIGEN PRECURSOR
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=94161746; PubMed=8117286;
 RA Sakurada C., Seno H., Dohi N., Takizawa H., Nonaka M., Okada N.,
 Okada H.;
 RT "Molecular cloning of the rat complement regulatory protein, 512
 antigen";
 RL Biochem. Biophys. Res. Commun. 198;819-826(1994).
 DR EMBL: D42114; BAA07698.1; -.
 DR HSSP: P10998; IYVD.
 DR INTERPRO: IPR000436; -.
 DR PFAM: PF00084; sushi; 6.
 KW Signal.
 FT SIGNAL 1 36 POTENTIAL.
 FT CHAIN 37 497 512 ANTIGEN.
 SQ SEQUENCE 497 AA; 54786 MW; 177AC1BE0F1ADIC CRC64;

Query Match 62.4%; Score 689; DB 11; Length 497;
 Best Local Similarity 64.3%; Pred. No. 7.2e-64;
 Matches 126; Conservative 17; Mismatches 53; Indels 0; Gaps 0;

QY 2 QCNAPWLPFARPTNLTDPEFPITGYLYNECRPGYSGRPSIICLKNSVWTGAKRRCR 61
 ID 063135 PRELIMINARY; PRT; 559 AA.
 AC Q63135;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE COMPLEMENT REGULATOR PROTEIN.
 GN CRRY.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE=96006570; PubMed=7590969;
 RA Ouyg R.J., Lo C.F., Alexander J.J., Sneed A.E., Moxley G. III;
 RT "Molecular characterization of rat Crry: widespread distribution of
 two alternative forms of Crry mRNA";
 RL Immunogenetics 42:362-367(1995).
 (2)
 RN SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Dohi N., Sakurada C., Nonaka M., Okada N., Okada H.;

RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U36532; AAA91821.1; -.
 DR EMBL: D42115; BAA22548.1; -.
 DR HSSP: P10998; IYVD.
 DR INTERPRO: IPR000436; -.
 DR PFAM: PF00084; sushi; 7.
 SQ SEQUENCE 559 AA; 61680 MW; 29FL0F6A21DB9B6E CRC64;

Query Match 62.4%; Score 689; DB 11; Length 559;
 Best Local Similarity 64.3%; Pred. No. 8.3e-64;
 Matches 126; Conservative 17; Mismatches 53; Indels 0; Gaps 0;

QY 2 QCNAPWLPFARPTNLTDPEFPITGYLYNECRPGYSGRPSIICLKNSVWTGAKRRCR 61
 ID 063135 PRELIMINARY; PRT; 162 AA.
 AC Q63135;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE COMPLEMENT RECEPTOR 1 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN SEQUENCE FROM N.A.
 RC MEDLINE=90110163; PubMed=2295627;
 RA Hourcade D., Mesner D.R., Bee C., Zeldes W., Atkinson J.P.;
 RT "Duplication and divergence of the amino-terminal coding region of the
 complement receptor 1 (CR1) gene. An example of concerted (horizontal)
 evolution within a gene";
 RL J. Biol. Chem. 265:974-980(1990).
 DR EMBL: M31241; AAD15289.1; JOINED.
 DR EMBL: M31238; AAD15289.1; JOINED.
 DR EMBL: M31239; AAD15289.1; JOINED.
 DR EMBL: M31240; AAD15289.1; JOINED.
 DR HSSP: P02749; IOUB.
 DR INTERPRO: IPR000436; -.
 DR PFAM: PF00084; sushi; 2.
 KW Receptor.
 FT NON_TER 162
 SQ SEQUENCE 162 AA; 17525 MW; B9362CAF8F8ED47 CRC64;

Query Match 61.7%; Score 681; DB 4; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.2e-63;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QCNAPWLPFARPTNLTDPEFPITGYLYNECRPGYSGRPSIICLKNSVWTGAKRRCR 61
 ID 063135 PRELIMINARY; PRT; 162 AA.
 AC Q63135;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE COMPLEMENT RECEPTOR 1 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN SEQUENCE FROM N.A.
 RC MEDLINE=90110163; PubMed=2295627;
 RA Hourcade D., Mesner D.R., Bee C., Zeldes W., Atkinson J.P.;
 RT "Duplication and divergence of the amino-terminal coding region of the
 complement receptor 1 (CR1) gene. An example of concerted (horizontal)
 evolution within a gene";
 RL J. Biol. Chem. 265:974-980(1990).
 DR EMBL: M31241; AAD15289.1; JOINED.
 DR EMBL: M31238; AAD15289.1; JOINED.
 DR EMBL: M31239; AAD15289.1; JOINED.
 DR EMBL: M31240; AAD15289.1; JOINED.
 DR HSSP: P02749; IOUB.
 DR INTERPRO: IPR000436; -.
 DR PFAM: PF00084; sushi; 2.
 KW Receptor.
 FT NON_TER 162
 SQ SEQUENCE 162 AA; 17525 MW; B9362CAF8F8ED47 CRC64;

OY 122 D 122
DB 162 D 162

RESULT 14

ID 099254 PRELIMINARY: PRT: 679 AA.

AC 099254:

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE COMPLEMENT RECEPTOR TYPE 2 (CR2) (FRAGMENT).

GN CR2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALE/C;

RA MEDLINE=90229754; PubMed=2139460;

RA Kurtz C.B., O'Toole E., Christensen S.M., Weis J.H.;

RT "The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene transcripts predicts two distinct gene products that share homologous domains with both human CR2 and CR1."

RL J. Immunol. 144:3581-3591(1990).

RN [2]

RP SEQUENCE OF 21-367 FROM N.A.

RA MEDLINE=95105691; PubMed=7528766;

RA Kim Y.O., Kinoshita T., Molina H., Hourcade D., Seya T., Wagner L.M.,

RA Holers V.M.;

RT "Mouse complement regulatory protein Cr1/p65 uses the specific mechanisms of both human decay-accelerating factor and membrane cofactor protein."

RL J. Exp. Med. 181:151-159(1995).

DR EMBL: U17128; AAA78271.1; -.

DR EMBL: U17123; AAA78271.1; JOINED.

DR EMBL: U17124; AAA78271.1; JOINED.

DR EMBL: U17125; AAA78271.1; JOINED.

DR EMBL: U17126; AAA78271.1; JOINED.

DR EMBL: U17127; AAA78271.1; JOINED.

DR EMBL: M36470; AAA37449.1; -.

DR HSSP: P10998; 1YVD.

DR MGD: MGI:88489; Cr2.

DR INTERPRO: IPR000436; -.

DR INTERPRO: IPR002386; -.

DR PFAM: PF00084; sush1. 10.

DR PRINTS: PRO0343; SELECTIN.

FT NON_TER 679

SQ SEQUENCE 679 AA; 74916 MW; 52FC0DFCED20CDC CRC64;

Query Match 56.5%; Score 624; DB 11; Length 679;

Best Local Similarity 56.8%; Pred. No. 6.7e-57;

Matches 109; Conservative 32; Mismatches 51; Indels 0; Gaps 0;

OY 2 OCNAPFEMLPFARPTNLTDEFEPIGTLYLNECRPGYSGRPFSTICLKNVWGAKDRCRR 61

DB 21 QCKLLPKYSFAKSIYSDKSEFAIGTWKCRPGFRKSFITTCLETSKMSDAQDFCKR 80

OY 62 KSCRNPDPVNGAVHYIKGIQFSGQIKYSCTKGKRLIGSSSACIIISGDTVIMDNFTFIC 121

DB 81 KPCMNQEPPLHGSVHINTGIEFSGTITTYSCNQGRLIGSSSACIYSDNTVMMDMFLC 140

OY 122 DRTPCLPTIANGDFTSISREYFHGVSVTYTCNLSGSKKVFELVGEISITCTSKDQ 161

DB 141 ESTIPCSPPAISNGDEYSSRSDFYGMVVTYYCHGKRNREKLFDLVGEKSIYCTSKNQ 200

OY 182 VGIMSGPAPOCI 193

DB 201 VGIMNSPPOCI 212

RESULT 15
ID 062479 PRELIMINARY: PRT: 330 AA.

AC 062479:

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE X/Y PROTEIN (FRAGMENT).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=87196375; PubMed=2952719;

RA Aegerter-Shaw M., Cole J.L., Klickstein L.B., Wong W.W., Fearon D.T.,

RA Lailey P.A., Weis J.H.;

RT "Expansion of the complement receptor gene family. Identification in the mouse of two new genes related to the CR1 and CR2 gene family."

RL J. Immunol. 138:3488-3494(1987).

DR EMBL: M16179; AAA40574.1; -.

DR HSSP: P10998; 1YVD.

DR INTERPRO: IPR000436; -.

DR INTERPRO: IPR001005; -.

DR PFAM: PF00084; sush1. 4.

DR PROSITE: PS00037; MYB.1; UNKNOWN_1.

FT NON_TER 1

SQ SEQUENCE 330 AA; 36568 MW; FE2A26A15F43B6F2 CRC64;

Query Match 42.9%; Score 474; DB 11; Length 330;

Best Local Similarity 62.0%; Pred. No. 1.4e-41;

Matches 85; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

OY 9 LPPARPNTLDEFEPIGTLYLNECRPGYSGRPFSTICLKNVWGAKDRCRRKSCRNP 68

DB 194 LPSAKRINTLDESMFPIGTLYLLECLPGYIKRQFSTICKQDSITWTSABEDCKRCKCKTS 253

OY 69 DPNNGAVHYIKGIQFSGQIKYSCTKGKRLIGSSSACIIISGDTVIMDNFTPIDRIPCL 128

DB 254 DPENGLVHVTGIEFSGRINTYTCNQGRLIGSSSACVITDSDVDTEAPICIEWIPCEI 313

OY 129 PPTIANGDFTSISREY 145

DB 314 PPGIANGDFTSISREDF 330

Search completed: January 13, 2001, 13:49:06
Job time: 390 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 12:26:35 ; Search time 1005.48 seconds
(without alignments)
4118.854 Million cell updates/sec

Title: US-09-380-682-2
Perfect score: 591
Sequence: 1 ATGCAGTGCACGCTCCGGA.....AGTGCATCATCCGACAA 591

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_est4:
5: gb_est5:
6: gb_est6:
7: gb_est7:
8: gb_est8:
9: gb_est9:
10: gb_est10:
11: gb_est11:
12: gb_est12:
13: gb_est13:
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 185: gb_est118:*
 186: gb_est119:*
 187: gb_est120:*
 188: gb_est121:*
 189: gb_est122:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Result No.	Score	Match	Length	DB	ID	Description
C 1	279.4	47.3	444	24	A1718588	A1718588 as46h01.x
C 2	267.4	45.2	465	109	BE552138	BE552138 hw29d02.x
C 3	263.2	44.5	650	93	AM610808	AM610808 up37f12.x
C 4	259.4	43.9	443	17	A1240881	A1240881 qj94e04.x
C 5	248	42.0	611	96	AM851015	AM851015 IL3-CT02
C 6	235.6	39.9	549	96	AM919879	AM919879 EST351183
C 7	215.2	36.4	356	24	A1735459	A1735459 att1h03.x
C 8	211.8	35.7	488	137	BE917021	BE917021 601663678
C 9	211.2	35.7	488	139	BE923537	BE923537 ux09c08.y
10	210	35.5	525	4	AA286570	AA286570 vb76a03.r
11	204	34.5	441	95	AM825298	AM825298 us13d06.y
12	203	34.3	614	2	AA107525	AA107525 mp08b07.r
13	197.6	33.4	601	3	AA212152	AA212152 mb80g07.r
14	191.4	32.4	684	3	AA186185	AA186185 mc63d04.r
15	187.6	31.7	654	17	A1194601	A1194601 ue65b04.r
16	174.4	29.5	389	145	T66823	T66823 ya50b08.s3
C 17	170.8	28.9	433	24	A1735085	A1735085 as44f09.x
C 18	168	28.4	643	96	AM912091	AM912091 u41f04.y
19	159.2	26.9	327	158	AO529858	AO529858 RPT-11-3
20	155.8	26.4	403	93	AM610947	AM610947 un74b11.y
21	155.8	26.4	409	38	AM012541	AM012541 u006c01.y
22	154.4	26.1	643	3	AA153888	AA153888 mq56d05.r
23	152	25.7	320	151	AQ266148	AQ266148 C1EB1-E1-
24	146.2	24.7	541	146	T83269	T83269 yd41a11.r1
25	144.4	24.0	387	87	AM211552	AM211552 uc82e02.y
26	142	24.0	346	145	T66824	T66824 ya50b08.r3
27	141.8	24.0	327	141	H31617	H31617 EST105833 R
28	140.2	23.7	469	4	AA261275	AA261275 vD03b10.r
29	135.2	22.9	613	106	BE308463	BE308463 601090308
30	134.8	22.8	544	4	AA271926	AA271926 vb75c04.r
31	129.4	21.9	355	145	T27695	T27695 EST12512 Hu
32	126.8	21.3	382	13	AA683947	AA683947 vx87p09.r
33	123.8	20.9	431	139	BF015454	BF015454 uy21g02.y
34	115	19.5	419	11	AA756782	AA756782 vv65f04.r
35	112.8	19.1	835	3	AA174888	AA174888 ms77g05.r
36	111.4	18.8	559	91	AM519788	AM519788 up39d05.y
37	109	18.4	550	91	AW502222	AW502222 ut-HF-BR0
38	105	17.8	440	142	H73873	H73873 ys14d08.r1
39	103	17.4	499	13	AA895111	AA895111 yv07b12.r
40	85.2	14.4	527	158	AQ492897	AQ492897 HS_5126.A
41	85	14.4	356	14	AA982230	AA982230 ua49b04.r
42	81	13.7	660	2	AA145452	AA145452 mr79g11.r
43	76	12.9	564	13	AA895456	AA895456 vx65a07.r
44	75	12.7	370	111	BE655649	BE655649 ut-M-BH0
45	73.6	12.5	388	10	AA655637	AA655637 vs43a01.r

ALIGNMENTS

RESULT 1
 A1718588/c
 LOCUS
 DEFINITION as46h01.x1 Barstead aorta HPLRB6 Homo sapiens CDNA clone
 IMAGE:2320273.3' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE
 1.PRECURSOR (HUMAN), mRNA sequence.
 ACCESSION A1718588
 VERSION A1718588
 KEYWORDS EST.
 GI:5035844
 EST
 10-JUN-1999

RESULT	2
BE552138/c	
LOCUS	
DEFINITION	BE552138 465 bp mRNA EST 10-AUG-2000 hw29602.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:318433 3'
ACCESSION	(HUMAN); mRNA sequence.
VERSION	BE552138
KEYWORDS	EST.
SOURCE	BE552138.1 GI:9793830
ORGANISM	human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 465)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
JOURNAL	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
COMMENT	Email: Robert.Strausberg@nih.gov Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov Seq primer: -40UP from Gibco High quality sequence stop: 456. Location/Qualifiers 1..465 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="3184323" /clone_id="NCI_CGAP_Kid1" /lab_host="DH10B" /note="Organ: Kidney; Vector: pUT73D-Pac (Pharmacia) with a modified polylinker, Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAI purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNA from a pool of 5,000 clones made from the same library (cloneds 1323376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo." Subtraction by Bento Soares and M.
BASE COUNT	134 a 85 c 107 g 139 t
ORIGIN	
Query Match	45.2% Score 267.4; DB 109; Length 465;
Best Local Similarity	83.3%; Pred. No. 3.6e-75;
Matches 304; Conservative	0; Mismatches 61; Indels 0; Gaps 0;
Db	
4	CAGTGCAACGCTCCGGATGCGCTGCCTCGGCCCGCAGCAACTGACTGTAATT 63
450	CAATGCATGTCCCGGAATGCGTCCTCCATTGGCAGCGCTACCAACTAAGTAGTACTTT 391
Db	
64	GAGTTCGGCATCGGACTACCTGAACACGAAATCCCGCGGGTTATAGCGGCCGCCG 123
390	GAGTTTCCCATTTGGACATATCTGAACATATAATGCCCCCTGGTTATTCGGAAGACC 331
QY	TTTTCTATCATCTGCGCTGAAAACCTCTCTCGAATGTGTGCTAAGGACCGTTGCCGAG 183
Db	TTTTCTATCATCTGCGCTAAAAAACTCACTCTGGACAAGTGGTAAAGACAAGTCAAACGT 271
QY	AAATCTGTCTAATCCGCCAGATCCGGTTAACGGCATGTGATGATCAAAAGGCAT 243

1

AI240881.1 443 bp mRNA EST 28-JAN-1999
 g9j9e04.x1 NCI-CGAP_Kid3 Homo sapiens CDNA clone IMAGE:1867134 3'
 Similar to gb|Y00816_cds1 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR
 (HUMAN); mRNA sequence.
 AI240881
 AI240881.1 GI:3836278
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 443)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1350
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLT at:
www.dio.lnll.gov/bdrp/image/image.html
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 High quality sequence: step: 373.
 Location/Qualifiers
 1. 443
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 /db_xref="taxon:9606"
 /clone="IMAGE:1867134"
 /clone_1lb="NCI-CGAP_Kid3"
 /lab_host="DH10B"
 /note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with

AUTHORS Lee, N.H., Glozek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
TITLE Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
src: .

OY	4	CAGGCAACGGTCCGGAAATGGTGCCTTGGCGCGCCGCAACACTGACATGATAATT	63
Db	24	CACGCCCCAGGCCCATACAGCTTCCTCTGCGCAACCTATAATTAATCATATGATTC	83
OY	64	GAGTTCOCGATCGGTACTACTCTGAACCTAGCAATGCGCCGCGGGTATATGCGCGCCCG	123
Db	84	ATGTTTCCCATGG---ACATATTGTGTATGATATGCTCCGAGATATATCAAGAGCAG	140
OY	124	TTTCTCTATCATCTCCCGAAAAACTGTGTGACTGCGTAAAGAACCGTCGCGCAGT	183
Db	141	TTCTCTATCACTGCAAAACAAGACTCACTGAGCAGGTCGTGAAATTAAGTGTATAGA	200
OY	184	AAATCTGTGCTAATCCGCAGATCCGGTTAACGCGCATGCTGATGATCAAAAGGCATC	243
Db	201	AAACAATGTAATAACTCTCTCAGATCCCGAANAAGCCTTGATCATGTAAACACAGGCATT	260
OY	244	CAGTTCGGTTCCTCCAAATAAATATCTTGTACTGAAAGGATTAACGCTGATTTGGTCCCC	303
Db	261	CAGTTTGGATCCGTATTAATTAATCTGTAATCAAGGATACCGCTCTATTGGTTCCTCC	320
OY	304	AGCCGTACATGCATCATCTCTGGTATGACTGCTATTGGGATTAATGAACACCCGATTGT	363

Query Match	35.7%;	Score 211.2;	DB 139;	Length 488;
Best Local Similarity	65.9%;	Pred. NO. 4.4e-57;		

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Matches 306; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

OY 4 CAGTGAACGCTCCGGAATGGCTGCGGTCGCGCCGACCAACCTGACTGATGATTT 63
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Db 9 CACTGCCAGCCCCCATCAGAGCTTCTTCTGCCAACCCTAATCTAATGATGATCC 68
OY 64 GAGTTCGCCATGGTACCTGACCTGAGATGAGATGCGCGGGTTATGCGGCCGCG 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 AGTTTCCCATTTGGAACATATTTGTTGTAATGCTCTCCAGATATATCAAGAGGCG 128
OY 124 TTTTCTATCATCTGCGCTGAAAACTCTGCTGAGCTGCTGCTAAGACCGTTGCCGAGT 183
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Db 129 TTTCTATCACCCTGCAAAACAGCTCAACCTGAGAGAGTGTGAAGATAGTATACGA 188
OY 184 AATATGTGCGTAATCCGCGACATCCGTTAAGCGCATGTCATGATCAAGGCATC 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 189 AATCATATGAACCTCTTCAAGATCTGAGATGGCTTGTACATGATACACAGGCAT 248
OY 244 CAGTTCGTTCCCAATTAATATTTCTTACTAAGGTTACGCTGATGGTCCCTCC 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 249 CAGTTTGGATCCCGATTAATATTAATCTTATCAAGATACCGCTCATTTGTTCTCC 308
OY 304 AGCGTACATCATCATCTCTGGTATACCTGCTATTGGGATATGAACACCGATTGT 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 309 TCTGCTGATGTCATCATCACTCAAGTGTGATGGATACAGGACCTATTGT 368
OY 364 GACCAATTCGCTGCTGCTGCGCGGACCATCGCCACAGGATTTCACTCTATCAGT 423
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Db 369 GAGTGGATTCCTGTGAGATACCCGACGACATTCCTCAATGGATTTCTTCTTCAAC 428
OY 424 CGCGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 467
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 429 AGAGAAGACTTCATTATGAGATGCTGTTACTTACCTACCGCTGCA 472

RESULT 10
AA286570 525 bp mRNA EST 09-APR-1997
LOCUS vb76a03.r1 Soares mouse 3NME12 5 Mus musculus cDNA clone
DEFINITION IMAGE:762892.5' similar to gb:M23529 Mus musculus complement
receptor (MOUSE);, mRNA sequence.
ACCESSION AA286570
VERSION AA286570.1 GI:1931666
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 525)
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 525)
Geisel,S., Kucaba,T., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Mesteron,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNC; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 489.
Location/Qualifiers
1..525
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

FEATURES
Source
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/organism="Mus musculus"
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/db_xref="taxon:10090"

Matches 312; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

Query Match 35.5%; Score 210; DB 4; Length 525;
Best Local Similarity 64.7%; Pred. No.1.1e-56;
Matches 312; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

OY 4 CAGTGAACGCTCCGGAATGGCTGCGGTCGCGCCGACCAACCTGACTGATGATTT 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 37 CACTGCCAGCCCCCATCAGAGCTTCTTCTGCCAACCCTAATCTAATGATGATCC 96
OY 64 GAGTTCGCCATGGTACCTGACCTGAGATGAGATGCGCGGGTTATGCGGCCGCG 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 97 AGTTTCCCATTTGGAACATATTTGTTGTAATGCTCTCCAGATATATCAAGAGGCG 156
OY 124 TTTTCTATCATCTGCGCTGAAAACTCTGCTGAGCTGCTGCTAAGACCGTTGCCGAGT 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 157 TTTCTATCACCCTGCAAAACAGCTCAACCTGAGAGAGTGTGAAGATAGTATACGA 216
OY 184 AATCTTGTGCTATCCGCCAGATCCGTTAAGCGATGCTGATGATCAAGGCATC 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 217 AATCAATGTAAACCTCTTCAAGATCCGAGAAATGGCTTGTGATCATGACACAGCAT 276
OY 244 CAGTTCGTTCCCAATTAATATTTCTTACTAAGGTTACGCTGATGGTCTCTCC 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 277 CAGTTTGGATCCCGATTAATATTAATCTTATCAAGATACCGCTCATTTGTTCTCC 336
OY 304 AGCGTACATCATCATCTCTGGTATACCTGCTATTGGGATATGAACACCGATTGT 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 337 TCTGCTGATGTCATCATCACTGATCAAGTGTGATGGAACTGAGGACCTATTGT 396
OY 364 GACCGATTCGCTGCTGCTGCGCGGACCATCGCCACAGGATTTCACTTATCAGT 423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 397 GAGTGGATTCCTGTGAGATACCCGACGACATTCCTCAATGAGATTTCTTCAAGTCA 456
OY 424 CGCGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 457 AGAGAAGACTTCATTATGAGATGCTGTTACTTACCGCTGCAACACTGATGCGAGG 516
OY 484 AA 485
Db 517 AA 518

RESULT 11
AA825298 441 bp mRNA EST 17-MAY-2000
LOCUS us13d06.y1 Soares NMBC_B-cell Mus musculus cDNA clone
DEFINITION IMAGE:3166955.5' similar to gb:M23529 Mus musculus complement
receptor (MOUSE);, mRNA sequence.
ACCESSION AA825298
VERSION AA825298.1 GI:7918375
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 441)
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Query Match	Score	DB	Length
33.48;	197.6;	3;	601;
Best Local Similarity	64.88;	Pred. No. 1.1e-52;	

TITLE	JOURNAL	COMMENT
The WashU-HM1 Mouse EST Project	Unpublished (1996)	
Contact: Marra M/Mouse EST Project		
WashU-HM1 Mouse EST Project		
Washington University School of Medicine		
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
Tel: 314 286 1800		
Fax: 314 286 1810		
Email: mouseest@watson.wustl.edu		
This clone is available royalty-free through LNL; contact the		
IMAGE Consortium (info@image.llnl.gov) for further information.		
MG1:386559		
Seq primer: -78M13 rev2 from Amersham		
High quality sequence scop: 451.		
Location/Qualifiers		
1..684		
/organism="Mus musculus"		
/strain="C57BL/6J"		


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/db_xref="taxon:10090"
/clone="IMAGE:634567"
/clone_lib="Soares_thymus_2nbm1"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5].
TGTATCCATATCTGAAGTGGAGGCGCCGTTTTTTTTTTTTTTTTTTTT
3'; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."

```

Query Match	32.4%	Score 191.4	DB 3	Length 684
Best Local Similarity	66.0%	Pred. 0.11e-50		
Matches 276	Conservative 0	Mismatches 142	Indels 0	Gaps 0
QY 174	TTGCCGAGTAATTTGCTGCTAATCCGCAATCCGGTTAAGCGCATGTCATGTCAT	233		
Db 208	TTTCATAGGAACAACATGTAACACTCTTCACATCTCTGAGATGGCTTGATCTTAA	267		
QY 234	CAAGGCAATCCAGTTCGGTTCCTCAATTAATATTTCTTGACTAAAGGTTACCGT	293		
Db 268	CACAGGCAATTCAGTTGGATCCCGTATTAATTAATCTTAAATCAAGATACCGCTCA	327		
QY 294	TGCTTCCTCCAGCGCTACATGCATCATCTCTGTGATACTGTCTTTGGGATATGAAC	353		
Db 328	TGGTTCCTCTCTGCTGTATGTGTATCATCTATCAAACTGTGATGGGATACCTAGCG	387		
QY 354	ACCGATTTGTGACCAATTCCTGTGTCGTGGCCGCGACATCGCCAGGATGATTCAC	413		
Db 388	ACCTATTTGTGATGTCATCTCTGTGATGATACCCGACGATCTCCAAATGGAGATTTCT	447		
QY 414	CTCTATCAGTCGCGAGTATTTTCAGTATGTTCTGTGTGATGACCTACACATCTGGG	473		
Db 448	CAGTTCACACAGAGAAGACTTCATATGATGAATGGGATTAAGTCTGACGCTGCAACATGA	507		
QY 474	TAGCGCTGGTAAAAAGGTCTTTGAGCTCTGTGGTGAAGCCGCTCATCTACTGACATG	533		
Db 508	TGCGAGAGGGAAGGCGCTCTTTTAACTGGTGGGTGAGCCCTCTTACTGTATACCA	567		
QY 534	AGACATCAAGTGGGCAATCTGAGAGCGCGCCGCGACCGCATGTCATATCCGCAACA	591		
Db 568	CGATGTGAGATTTGAGTCTGGNAGCGGCTCTCTCTCAGTGCATGAACCTCAACAA	625		

RESULT 15

LOCUS A1194601

DEFINITION A1194601 654 bp mRNA EST 14-OCT-1998

DESCRIPTION use95b04.r1 Soares_NMPu Mus musculus cDNA clone IMAGE:1496335 5' similar to gb:Y00816.cdsl COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (HUMAN); gb:M23529 Mus musculus complement receptor (HOUSE);, mRNA sequence.

ACCESSION A1194601

VERSION A1194601.1 GI:3747207

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 654)

AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thetling, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

TITLE Waterston,R.
JOURNAL The WashU-HHMI Mouse EST Project
COMMENT Unpublished (1996)
Contact: Maria W/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@waterston.wustl.edu
This clone is available royalty-free through LINL ; contact the
IMAGE Consortium (info@image.linnl.gov) for further information.
MGI:933939
Trace considered overall poor quality
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence strip: 1.
Location/Qualifiers
1..654
/organism="Mus musculus"

/note="Organ: uterus: Vector: PT733D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
 BASE COUNT
 ORIGIN
 164 a 132 c 179 g 177 t 2 others

Query Match	31.7%	Score 187.6	DB 17	Length 654
Best Local Similarity	66.7%	Pred. No. 1.9e-49		
Matches 268	Conservative 0	Mismatches 133	Indels 0	Gaps 0
QY 161	GTGCTAAGACCGTGGCCAGAGTAATCTGTGTAATCCGGCAGATCCGGTTAAGGCA	220		
Db 2	GTGCTAGAGATAAGTATACGAAACATGTAAACCTCTTCAGATCGTAGAATGGCT	61		
QY 221	TGTGTCAATGTATCAAAAGCATCCAGTTCGGTTCCTCCAAATTAATCTTGTACTAAG	280		
Db 62	TGTGTCAATGTATCAAAAGCATCCAGTTCGGTTCCTCCAAATTAATCTTGTACTAAG	121		
QY 281	GTTACCGTGTGTTGGTTCCTCCAGCGGTACATCATCTCTGGTACTGATCTT	340		
Db 122	GATACGGCTCATATGGTTCCTCCTCTGCTGTATATGTGTCTACTATCAAAATGTTGANT	181		
QY 341	GGGATATGAAACACCGCATTTGTGTACCGAATTCGCTGTGTCTGCCGCCACATCGCCA	400		
Db 182	GGGATGCTGAGGACCACTTTTGTGTGATGATCTCTCTGTAGATACCCCGAGCATTTCCA	241		
QY 401	ACGGATTTTCAACCTCTATCAAGTCGCGAGATTTTCACTATAGTCTGTGGTACTACC	460		
Db 242	ATGGAGATTTTCTTCAGTTCACACCGAGAGAAAGATTTCATTATGGAATGTGTACTACC	301		
QY 461	ACTGCATCTGGGTAGCCGTGGTAAAAAGGTGTTAGACTCGTGGGTAGCCGCTCATCT	520		
Db 302	GCTGCACACTGATGTCGAGAGAGGAGGCGCTTTAACTGGTGGTGAGCCCTCTTAT	361		
QY 521	ACTGCATCTAGCAAAAGACATCAAGTGGGCACTGTGAGCGGCC	582		
Db 362	ACTGTACGACGACGATGTTGAATTTGAGTGTGAGCGGCC	403		

Search completed: January 13, 2001, 12:50:01
Job time: 1406 sec

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